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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the heart and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

CROSS REFERENCE TO RELATED APPLICATIONS

5 The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S.provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20 The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_HEART.txt, created
25 24 January 2001, having 20,186,946 bytes. The Sequence
Listing contained in said file on said disc is incorporated
herein by reference in its entirety.

Field of the Invention

30 The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known a priori with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only a priori biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
sequence information from multiple genera, from multiple
20 species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies. There is a need for methods
25 and apparatus that permit prediction, diagnosis and prognosis of diseases of the human heart, particularly those diseases with polygenic etiology.

Summary of the Invention

30

 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present
35 invention also provides apparatus for verifying the

expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human heart, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 19,771 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 9,981 - 19,771, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 9,980.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOS.: 1 - 9,980 or a complementary sequence or a fragment thereof
30 wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOS.: 9,981
35 - 19,771 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding
5 a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

Preferably, a single exon nucleic acid probe in
10 accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or
15 preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length.
20 It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in
25 accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid
30 probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those
35 skilled in the art.

In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a
5 single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition,
10 comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;
wherein said at least one primer is sufficient to
15 prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in
20 accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each
25 probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from
30 genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said
35 probe is a single exon probe having a fragment identical in

sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at
5 high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic
10 sequence in accordance with the seventh aspect of the invention; and then

measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe
15 with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

20 In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 19,771 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a
25 sequence as set out in any of SEQ ID NOS: 9,981 - 19,771, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 - 9,980.

30 In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ ID NOS.: 9,981 - 19,771.

Accordingly in a eleventh aspect of the invention
35 there is provided a peptide comprising a sequence as set

out in any of SEQ ID NOs: 19,772 - 29,119, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

10

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic

acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

5 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the
10 larger nucleic acid molecule.

 As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

15 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

20 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9
25 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

 As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means
30 any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

 As used herein, a "Mondrian" means a visual
35 display in which a single genomic sequence is annotated

with predicted and experimentally confirmed functional information.

5 Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

10 FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence
15 data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

20 FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted
25 lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray.
30 The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

FIG. 7 is a pictorial representation of the
35 expression of verified sequences that showed expression

with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present

invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records 5 corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector 10 sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence 15 identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. 20 Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in 25 information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the 30 htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than 35 human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C.*

brigsii, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification

and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps

can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

5 Genomic sequence database 100 is first queried 20 for genomic sequence.

 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

10 For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process
15 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into
20 process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

 The exact content of query 20 will also depend upon the database queried. For example, if the database
25 contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

30 Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

35 For example, if the function sought to be

identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added

relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

5 One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further
10 described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of
15 the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

 If query 20 incorporates multiple criteria, such
20 as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

25 If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query
30 20 can be generated that takes into account the initial negative result.

 When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired
35 analytical approach and the particular analytical methods

thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized

by the subsequent bioinformatic algorithms, such as "X". Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

5 Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those
10 nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can also or alternatively be valued by presence in the longest contig.

 Preprocessing 24 can, and often will, also
15 include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25. Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence
20 database 100, or newly applied, and can further include additional annotation. Formatting can include conversion from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

25 Preprocessing, which can be optional depending upon the function desired to be identified and the informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified
30 within the genomic sequence.

 As mentioned above, such functions can include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after
35 transcription, of regulating message degradation, and the

like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

5 The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not
10 hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

15 Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

20 Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be
25 performed using any of a variety of known programs that identify regions with lower sequence variability.

 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in
30 Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

35 Increased reliability can be obtained when

consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

5 Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative

sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the
5 predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

10 Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

15 In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

20 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that
25 have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses
30 amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully
35 to amplify. Where subsequent gene expression assay relies

upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in

process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also
5 be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic
10 sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100
15 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from
20 application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an
25 approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the
30 methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it has been discovered that the percentage success at
amplifying pieces of such ORFs is low, and that such
35 putative exons are more effectively amplified when larger

fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as
5 PRIMER3 (available online for use at
<http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of
10 genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can
15 be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of
20 primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The
25 common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming
30 sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been
35 obtained, or a closely related species, and can

conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline

silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, 5 polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly 10 advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more 15 typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying 20 nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, 25 Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. 30 For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of 35 background noise in such microarrays.

As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or
5 alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose
10 certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the
15 expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed
20 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in
25 Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography
30 techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at
35 least 1000, typically at least 2000, preferably 5000 and

upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the
5 array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence,
10 representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and
15 advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for
20 study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be
25 derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such
30 microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed
35 genes. Furthermore, such libraries - and thus microarrays

based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

5 Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as
10 probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other
15 expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful
20 cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the
25 genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the
30 desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

35 Thus, the genome-derived single exon microarrays

of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin
5 from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the
10 homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message
15 polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein
20 as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material.
25 Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the
30 genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60,
35 70 or 80% or more of individual exon-including probes

disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-
5 including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence
10 of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or
15 amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays
20 need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is,
25 independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include
30 artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would
35 contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding
5 region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression
10 measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a
15 single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the
20 average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-
25 spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95
30 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the
35 probes in the genome-derived single exon microarrays of the

present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or
5 include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in
10 turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in
15 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon
20 microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST
25 microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional
30 presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay spliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the
35 present invention are also quite different from *in situ*

synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

5 A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe
10 basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays
15 from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al.,
20 *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent
25 use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence
30 drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred
35 embodiments, the methods and apparatus of the present

invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

- 5 After the physical substrate is prepared, experimental verification of predicted function is performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental
10 verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon
15 microarrays prepared as above- described.

Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the
20 microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous,
25 as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-
30 transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the
35 reference source is reverse transcribed in the presence of

a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial
5 purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a
10 Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the
15 genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support
20 substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention
25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is
30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates
35 having 384, 864, 1536, 3456, 6144, or 9600 wells, and

although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

5 In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such
10 as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
15 in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers,
20 etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together
25 with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

30 In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable
35 media can be packaged with the microarray, with the ordered

probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification
10 sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted
15 to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than,
20 or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

25 Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and
30 more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - including information on identical sequences and
35 information on nonidentical sequences that have diffuse or

focal regions of sequence homology to the query sequence — can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

5 Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully
10 relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are
15 well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present
20 invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

25 FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

30 Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual
35 nucleotides would rarely be readable in hard copy output of

display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and

last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select

a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs
5 (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with
10 the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display
15 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the
25 present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As
30 noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of
35 bioinformatic assay of the genomic sequence. For example,

where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof.

5 As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked

10 information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

15 Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

20 Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the

25 degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for

30 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute

35 expression (signal intensity) can be expressed using

normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of

portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from
5 previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic
10 acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human
15 genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 9,980 of these ORFs in heart.

As would immediately be appreciated by one of
20 skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in heart.

Diseases of the heart and vascular system are a
25 significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as
30 causative, these disorders are for the most part believed to have polygenic etiologies.

For example, cardiovascular disease (CVD), which includes coronary heart disease, stroke, and peripheral arterial vascular disease, is the leading cause of death in
35 the United States and other developed countries. In

developing regions, coronary heart disease and stroke are ranked second and third, respectively, as causes of mortality. In the United States alone, about 1 million deaths (about 42% of total deaths per year) result from CVD each year. CVD is also a significant cause of morbidity, with about 1.5 million people suffering myocardial infarction, and about 500,000 suffering strokes in the United States each year. With risk for CVD increasing with age, and an increasingly aging population, CVD will continue to be a major health problem into the future.

CVD is caused by arterial lesions that begin as fatty streaks, which consist of lipid-laden foam cells, and develop into fibrous plaques. The atherosclerotic plaque may grow slowly, and over several decades may produce a severe stenosis or result in arterial occlusion. Some plaques are stable, but other, more unstable, ones may rupture and induce thrombosis. The thrombi may embolize, rapidly occluding the lumen and leading to myocardial infarction or acute ischemic syndrome.

Risk factors for CVD include age and gender. In addition, a family history of CVD significantly increases risk, indicating a genetic basis for development of this disease complex. Obesity, especially truncal obesity, the cause of which is suspected to be genetic, is yet another risk factor for CVD. Familial disorders such as hyperlipidemia, hypoalphalipoproteinemia, hypertriglyceridemia, hypercholesterolemia, hyperinsulinemia, homocystinuria, and dysbetalipoproteinemia, all of which lead to lipid or lipoprotein abnormalities, can predispose one to the development of CVD. Both insulin-dependent and non-insulin-dependent diabetes mellitus, both of which have genetic components, have been also linked to the development of atherosclerosis.

The literature is replete with evidence for

genetic causes of cardiovascular diseases. For example, studies by Allayee et al., *Am. J. Hum. Genet.* 63:577-585(1998), indicated a genetic association between familial combined hyperlipidemia (FCHL) and small dense LDL particles. The studies also concluded that the genetic determinants for LDL particle size are shared, at least in part, among FCHL families and the more general population at risk for CVD. Juo et al., *Am. J. Hum. Genet.* 63: 586-594 (1998) demonstrated that small, dense LDL particles and elevated apolipoprotein B levels, both of which are commonly found in members of FCHL families, share a common major gene plus individual polygenic components.

The common major gene was estimated to explain 37% of the variants of adjusted LDL particle size and 23% of the variants of adjusted apoB levels.

The atherogenic lipoprotein phenotype (ALP) is a common heritable trait, symptoms of which include a prevalence of small, dense LDL particles, increased levels of triglyceride-rich lipoproteins, reduced levels of high density lipoprotein, and increased risk of CVD, particularly myocardial infarction. Both Nishina et al., *Proc. Nat. Acad. Sci.* 89: 708-712 (1992) and Rotter et al., *Am. J. Hum. Genet.* 58: 585-594(1996) demonstrated linkage between ALP and the LDLR locus. Rotter et al., *supra*, also reported linkage to the CETP locus on chromosome 16 and to the SOD1 locus on chromosome 6, and possibly also to the APOA1/APOC3/APOA4 cluster on chromosome 11.

Mutations in genes identified as components of lipid metabolism, e.g., apolipoprotein E (apoE) and LDL receptor (LDLR), have been shown to be associated with predisposition to the development of CVD. For example, several apoE variants had been found to be associated with familial dysbetalipoproteinemia, characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis (de Knijff et al., *Mutat* 4: 178-

194 (1994)). Mutations in the LDLR gene have been associated with the familial hypercholesterolemia, an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL),
5 that can lead to increased susceptibility to CVD.

To date, mutations in numerous genes have been shown to be associated with increased CVD susceptibility. However, the identified genetic associations are believed not to account for all genetic contributions to CVD.

10 As yet another example, hypertension is a major health problem because of its high prevalence and its association with increased risk of CVD. Approximately 25% of all adults and over 60% of persons older than 60 years in the United States have high blood pressure.

15 Arterial or systemic hypertension is diagnosed when the average of two or more diastolic BP measurements on at least two subsequent visits is 90 mm Hg or more, or when the average of multiple systolic BP readings on two or more subsequent visits is consistently greater than 140 mm
20 Hg. Pulmonary hypertension is defined as pressure within the pulmonary arterial system elevated above the normal range; pulmonary hypertension may lead to right ventricle (RV) failure.

Hypertension, together with other cardiovascular
25 risk factors, leads to atherosclerosis and other forms of CVD, primarily by damaging the vascular endothelium. In more than 40% of the U.S. population, hypertension is accompanied by hyperlipidemia and leads to the development of atherosclerotic plaques. In the absence of
30 hyperlipidemia, intimal thickening occurs. Non-atherosclerotic hypertension-induced vascular damage can lead to stroke or heart failure.

Familial diseases associated with secondary hypertension include familial renal disease, polycystic
35 kidney disease, medullary thyroid cancer, pheochromocytoma,

and hyperparathyroidism. Hypertension is also twice as common in patients with diabetes mellitus.

More than 95% of all hypertension cases are essential hypertension, that is, lack identifiable antecedent clinical cause. Essential hypertension shows clustering in families and can result from a variety of genetic diseases. In most cases, high blood pressure results from a complex interaction of factors with both genetic and environmental components. The recent search for genes that contribute to the development of essential hypertension has shown that the disorder is polygenic in origin. However, with several exceptions (such as angiotensinogen, angiotensin receptor-1, beta-3 subunit of guanine nucleotide-binding protein, tumor necrosis factor receptor-2, and "-adducin), the particular genes involved are still being sought.

Susceptibility loci for essential hypertension have been mapped to chromosomes 17 and 15q. Hasstedt et al., Am. J. Hum. Genet. 43: 14-22 (1988) measured red cell sodium in 1,800 normotensive members of 16 Utah pedigrees ascertained through hypertensive or normotensive probands, siblings with early stroke death, or brothers with early coronary disease, and suggested that red blood cell sodium was determined by 4 alleles at a single locus. This major locus was thought to explain 29% of the variance in red cell sodium, and polygenic inheritance explained another 54.6%. A higher frequency of the high red blood cell sodium genotype in pedigrees in which the proband was hypertensive rather than normotensive provided evidence that this major locus increases susceptibility to hypertension.

From a study of systolic blood pressure in 278 pedigrees, Perusse et al., Am. J. Hum. Genet. 49: 94-105 (1991) reported that variability in systolic blood pressure is likely influenced by allelic variation of a single gene, with gender and age dependence. They also suggested that a

single gene may be associated with a steeper increase of blood pressure with age among males and females.

There is strong evidence, however, for additional as yet uncharacterized, hypertension-associated loci on
5 other chromosomes.

For example, Xu et al., Am. J. Hum. Genet. 64: 1694-1701 (1999) carried out a systematic search for chromosomal regions containing genes that regulate blood pressure by scanning the entire autosomal genome using 367
10 polymorphic markers. Because of the sampling design, the number of sib pairs, and the availability of genotyped parents, this study represented one of the most powerful of its kind. Although no regions achieved a 5% genomewide significance level, maximum lod scores were greater than
15 2.0 for regions of chromosomes 3, 11, 15, 16, and 17.

As another example, cardiac arrhythmias account for several thousand deaths each year. Arrhythmias such as ventricular fibrillation, which causes more than 300,000 sudden deaths annually in the United States alone,
20 encompass a multitude of disorders. Another type of arrhythmia, idiopathic dilated cardiomyopathy, of which familial dilated cardiomyopathy accounts for 20-25%, is responsible for more than 10,000 deaths in the United States annually and is the predominant indication for
25 cardiac transplantation.

Cardiac arrhythmias can be divided into bradyarrhythmias (slowed rhythms) or tachyarrhythmias (speeded rhythms). Bradyarrhythmias result from abnormalities of intrinsic automatic behavior or
30 conduction, primarily within the atrioventricular node and the His-Purkinje's network. Tachyarrhythmias are caused by altered automaticity, reentry, or triggered automaticity.

Bradyarrhythmias arising from suspected polygenic disorders include Long QT syndrome 4, atrioventricular
35 block, familial sinus node disease, progressive cardiac

conduction defect, and familial cardiomyopathy.

Tachyarrhythmias with possible underlying polygenic causes include familial ventricular tachycardia, Wolff-Parkinson-White syndrome, familial arrhythmogenic right ventricular dysplasia, heart-hand syndrome V, Mal de Meleda, familial ventricular fibrillation, and familial noncompaction of left ventricular myocardium.

For some of the arrhythmias, one or more of the causative genes have been identified.

For example, atrioventricular block has been associated with mutations in the SCN5A gene, as well as mutations in a locus mapped to 19q13. Studies have shown linkage of familial sinus node disease to a marker on 10q22-q24. Familial ventricular tachycardia has been linked to mutations in genes encoding the G protein subunit alpha-i2 (GNAI1), and/or related genes. Examination of families with Wolff-Parkinson-White syndrome suggest an autosomal dominant pattern of inheritance and evidence of linkage of the disorder to DNA markers on band 7q3. Linkage analysis shows strong evidence for localization of a gene for Mal de Meleda disease on 8qter. Familial ventricular fibrillation can be caused by mutations in the cardiac sodium channel gene SCN5A. Familial noncompaction of left ventricular myocardium has been linked to mutations in the gene encoding tafazzin (TAZ), or in the FK506-binding protein 1A gene (FKBP1A).

Familial dilated cardiomyopathy is characterized by an autosomal dominant pattern of inheritance with age-related penetrance. The linkage of familial dilated cardiomyopathy to several loci indicate that it is polygenic. These loci include CMD1A on 1p11-q11, CMD1B on 9q13, CMD1C on 10q21, CMD1D on 1q32, CMD1E on 3p, CMD1F on 6q, CMD1G on 2q31, CMD1H on 2q14-q22, and CMD1I, which results from mutation in the DES gene on 2q35.

In addition, cardiomyopathy can also be caused by

mutations in the ACTC gene, the cardiac beta-myosin heavy chain gene (MYH7), or the cardiac troponin T gene.

Familial arrhythmogenic right ventricular dysplasia is inherited as an autosomal dominant with reduced penetrance and is one of the major genetic causes of juvenile sudden death. It is estimated that the prevalence of familial arrhythmogenic right ventricular dysplasia ranges from 6 per 10,000 in the general population to 4.4 per 1,000 in some areas.

Several loci for familial arrhythmogenic right ventricular dysplasia have been mapped indicating that this disease is also polygenic in nature. These loci include ARVD1 on 14q23-q24, ARVD2 on 1q42-q43, ARVD3 on 14q12-q22, ARVD4 on 2q32.1-q32.3, ARVD5 on 3p23, and ARVD6 on 10p14-p12.

Progressive cardiac conduction defect (PCCD), also called Lenegre-Lev disease, is one of the most common cardiac conduction diseases. It is characterized by progressive alteration of cardiac conduction through the His-Purkinje system with right or left bundle branch block and widening of QRS complexes, leading to complete atrioventricular block and ultimately causing syncope and sudden death. It represents the major cause of pacemaker implantation in the world (0.15 implantations per 1,000 inhabitants per year in developed countries). The cause of PCCD is unknown but familial cases with right bundle branch block have been reported suggesting that at least some cases are of genetic origin. Reports have linked PCCD to HBI on 19q13.3, and to mutations in the SCN5A gene (Schott et al., Nature Genet. 23: 20-21 (1999)).

As yet a further example, congenital heart disease occurs at a rate of 8 per 1000 live births, which corresponds to approximately 32,000 infants with newly diagnosed congenital heart disease each year in the United States. Twenty percent of infants with congenital heart

disease die within the first year of life. Approximately 80% of the first-year survivors live to reach adulthood. Congenital heart disease also has economic impact due to the estimated 20,000 surgical procedures performed to correct circulatory defects in these patients. The estimated number of adults with congenital heart disease in the United States is currently about 900,000.

In 90% of patients, congenital heart disease is attributable to multifactorial inheritance. Only 5-10% of malformations are due to primary genetic factors, which are either chromosomal or a result of a single mutant gene.

The most common congenital heart disease found in adults is bicuspid aortic valve. This defect occurs in 2% of the general population and accounts for approximately 50% of operated cases of aortic stenosis in adults. Atrial septal defect is responsible for 30-40% of congenital heart disease seen in adults. The most common congenital cardiac defect observed in the pediatric population is ventricular septal defect, which accounts for 15-20% of all congenital lesions. Tetralogy of Fallot is the most common cyanotic congenital anomaly observed in adults. Other congenital heart diseases include Eisenmenger's syndrome, patent ductus arteriosus, pulmonary stenosis, coarctation of the aorta, transposition of the great arteries, tricuspid atresia, univentricular heart, Ebstein's anomaly, and double-outlet right ventricle.

A number of studies have identified putative genetic loci associated with one or more congenital heart diseases.

Congenital heart disease affects more than 40% of all Down syndrome patients. The candidate chromosomal region containing the putative gene or genes for congenital heart disease associated with Down syndrome is 21q22.2-q22.3, between ETS2 and MX1.

DiGeorge syndrome (DGS) is characterized by

several symptoms including outflow tract defects of the heart such as teratology of Fallot. Most cases result from a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome region, or DGCR). The 22q11 deletion is the
5 second most common cause of congenital heart disease after Down syndrome. Several genes are lost in this deletion including the putative transcription factor *TUPLE1*. This deletion is associated with a variety of phenotypes, e.g., Shprintzen syndrome; conotruncal anomaly face (or Takao
10 syndrome); and isolated outflow tract defects of the heart including Tetralogy of Fallot, truncus arteriosus, and interrupted aortic arch.

Whereas 90% of cases of DGS may now be attributed to a 22q11 deletion, other associated chromosome defects
15 have been identified. For example, Greenberg et al., *Am. J. Hum. Genet.* 43:605-611 (1988), reported 1 case of DGS with del10p13 and one with a 18q21.33 deletion. Fukushima et al., *Am. J. Hum. Genet.* 51 (suppl.):A80 (1992) reported linkage with a deletion of 4q21.3-q25. Gottlieb et al.,
20 *Am. J. Hum. Genet.* 62: 495-498 (1998) concluded that the deletion of more than 1 region on 10p could be associated with the DGS phenotype. The association of the DiGeorge syndrome with at least 2 and possibly more chromosomal locations suggests strongly the involvement of several
25 genes in this disease.

Digilio et al., *J. Med. Genet.* 34: 188-190 (1997), calculated empiric risk figures for recurrence of isolated Tetralogy of Fallot in families after exclusion of del(22q11), and concluded that gene(s) different from those
30 located on 22q11 must be involved in causing familial aggregation of nonsyndromic Tetralogy of Fallot. Johnson et al., *Am. J. Med. Genet.* (1997) conducted a cytogenetic evaluation of 159 cases of Tetralogy of Fallot. They reported that a del(22q11) was identified in 14% who
35 underwent fluorescence in situ hybridization (FISH) testing

with the N25 cosmid probe.

Other congenital heart disease are also suspected to be of polygenic origin. For example, Holmes et al., Birth Defects Orig. Art. Ser. X(4): 228-230 (1974) described familial clustering of hypoplastic left heart syndrome in siblings consistent with multifactorial causation.

Other significant diseases of the heart and vascular system are also believed to have a genetic, typically polygenic, etiological component. These diseases include, for example, hypoplastic left heart syndrome, cardiac valvular dysplasia, Pfeiffer cardiocranial syndrome, oculofaciocardiodental syndrome, Kapur-Toriello syndrome, Sonoda syndrome, Ohdo Blepharophimosis syndrome, heart-hand syndrome, Pierre-Robin syndrome, Hirschsprung disease, Kousseff syndrome, Grange occlusive arterial syndrome, Kearns-Sayre syndrome, Kartagener syndrome, Alagille syndrome, Ritscher-Schinzel syndrome, Ivemark syndrome, Young-Simpson syndrome, hemochromatosis, Holzgreve syndrome, Barth syndrome, Smith-Lemli-Opitz syndrome, glycogen storage disease, Gaucher-like disease, Fabry disease, Lowry-Maclean syndrome, Rett syndrome, Opitz syndrome, Marfan syndrome, Miller-Dieker lissencephaly syndrome, mucopolysaccharidosis, Bruada syndrome, humerospinal dysostosis, Phaver syndrome, McDonough syndrome, Marfanoid hypermobility syndrome, atransferrinemia, Cornelia de Lange syndrome, Leopard syndrome, Diamond-Blackfan anemia, Steinfeld syndrome, progeria, and Williams-Beuren syndrome.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human heart and vascular system, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be

expressed at detectable levels in human heart, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

5 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known
10 to be characteristic of a given heart or vascular disease, or to specific grades or stages thereof.

 In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
15 patient's heart or vascular tissues to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in heart or vascular tissue of individuals with
20 known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

 In another approach, the genome-derived single
25 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of heart or vascular disease to be assessed through the massively parallel
30 determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human heart. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

35 The utility is specific to the probe; at

sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel *et al.* and Maniatis *et al.* — each probe reports the level of expression of message specifically containing that ORF.

5 It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

10 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
15 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
20 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
25 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
30 that are currently available for achieving these utilities.

 The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
35 for surveying gene expression in the human.

Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. Nature 405, 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and

Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney *et al.*, "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
46(3):425-8 (1999)), in drug discovery screens (see, for
5 example, Scherf *et al.*, "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi *et al.*, "*In vivo* Gene
Expression Profile Analysis of Human Breast Cancer
10 Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
appreciated that even those probes that show no change in
15 expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
failure of the agent to change a gene's expression level is
20 evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
lead compound discovery or in subsequent screening of lead
25 compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

WO 99/58720 provides methods for quantifying the
30 relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
percentage of the individual gene expression measurements
35 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

5 The invention particularly provides genome-derived single-exon probes known to be expressed in heart.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
10 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
15 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
20 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
25 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
30 amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
35 to be provided in a form suitable for amplification, the

range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
5 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
15 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
20 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
25 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
30 single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a
35 hybridization reaction in which the probe is not first

bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

5 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
10 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

15 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,981 - 19,771, respectively, for probe SEQ ID NOS. 1 - 9,980. The minimum amount of ORF required to be
20 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,981 - 19,771 individually by routine experimentation using standard high stringency
25 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
30 poly(dA), 0.2 µg/µl human c₀t1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high
35 stringency conditions can usefully be aqueous hybridization

at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have sequence complementary to those described herein above and

below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

- The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

- And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

- Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

- The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

- When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,980.

When used for gene expression analysis, the

genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from

10 a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the

15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as

20 probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,980 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,981 - 19,771, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,980 can be

25 used, or that portion thereof in SEQ ID NOS. 9,981 - 19,771 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

30 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo

35 Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New

England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,981 - 19,771. Such amino acid sequences are set out in SEQ ID NOS: 19,772 - 29,119. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method
5 approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support
10 substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF
15 was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was
20 commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to
25 add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon
30 to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR®
35 green (Molecular Probes, Inc., Eugene, OR) staining of

agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

5 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue
10 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 \pm 25 bp, approximately 50% of the average PCR
15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR
20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene
25 finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular
30 Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence
35 or the inclusion of vector and host contamination in some

submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent
5 empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was
10 observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using
15 commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of
20 background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified)
25 produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of
30 the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt
35 database using BLASTX, Gish et al., *Nature Genet.* 3:266

(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5 Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
116	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

10

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

15

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 5 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in 10 each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia 15 Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After 20 snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. 25 After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

30 Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 35 µg/µl human c₆t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant
5 signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single
10 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of
15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the
20 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using
25 the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-
30 05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were
35 identified; in heart, 150. The remaining tissues gave the

following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since

very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large
5 number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA
10 library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to
15 assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic
20 sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific
25 gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies,
30 Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two
35 sequences confirmed the tissue-specific gene expression as

measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
--

Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
 5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi *et al.*, *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998))(AC007320-3). A low homology analog (AF00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION 5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene 10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the 15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease 20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, 25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S
ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4

Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in heart tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,980 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 9,980 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,980. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons
30 present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,981 - 19,771, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the
5 signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15 Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations
20 are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered
25 to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that
30 particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

35 The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be
5 useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,981 - 19,771 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to
10 identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenomic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX)
15 expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as
20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the
25 SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:") from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of
30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is
35 found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, *e.g.*, less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 9,980) and probe exon (SEQ ID NOs.: 9,981 - 19,771, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

.. (a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human heart.

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit/Accession No.	Top Hit Database Source	Top Hit Descriptor
442	10396	20209	4.41				
871	10797	20647	17.08				
1029	10947		2.14				
1280	11186	21039	7.97				
1597	11501	21361	1.87				
1694	11523	21381	4.97				
1694	11596	21487	1.01				
1715	11616	21485	0.85				
1721	11622	21491	7.45				
1848	11744	21690	0.88				
1935	11830	21713	3.03				
2119	12005	21807	2.62				
2233	12116	22020	2.34				
3148	13074	22875	3.77				
3403	13320	23121	1.62				
3471	13397	23192	8.97				
3513	13429		0.87				
3607	13521	23309	0.69				
4102	14002	23781	1.71				
4164	14064	23838	5.64				
4184	14084	23958	0.89				
4184	14084	23959	0.89				
4242	14141		1.03				
4730	14816	24402	1.76				
4779	14903		0.79				
4876	14951	24917	5.08				
4983	14983	24929	2.07				
5217	15140	24934	1.92				
5217	15140	24935	1.92				
5328	15248		5				
5436	15356		5.89				
5483	15348		4.9				
5509	15427	25490	2.8				
5585	15451	25578	1.9				

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
5900	15599	25700	1.41			
5903	15709		1.54			
6342	18244	28404	1.61			
6342	18244	28405	1.51			
6937	19577	28769	1.29			
6942	19520	27012	1.3			
7494	17364	27599	3.68			
7694	17534	27748	1.26			
8070	17961		3.7			
8219	19472	28365	2.31			
8300	18299		2.54			
8699	18556	28840	2.91			
8737	17909	28130	1.73			
8737	17909	28151	1.73			
8732	18008		2.19			
9404	18094		1.62			
9700	18280	28220	2.11			
9897	15600	25701	13.31	6.9E+00 AJ235028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
9899	18548	28748	1.54	6.9E+00 U52716.1	NT	Human influenza A virus, partial, complete genome
7695	17805	28046	1.32	6.9E+00 AF242432.1	NT	Mus musculus Naip3 gene, exon 1, neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gt2H2) genes, complete cds
7695	17805	28047	1.32	6.9E+00 AF242432.1	NT	Mus musculus Naip3 gene, exon 1, neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1H polypeptide 2 (Gt2H2) genes, complete cds
2631	12499	22369	2.72	6.4E+00 L11433.1	NT	Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2631	12499	22380	2.72	6.4E+00 L11433.1	NT	Dengue virus type 3 membrane protein (prM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2693	12820	22012	5.61	6.4E+00 AB043785.1	NT	Mus musculus A19 gene for anitrombin, complete cds
7206	17093	27271	2.67	9.8E+00 P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP86)
5239	15163	24942	2.07	6.1E+00 AF066006.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5239	15163	24943	2.07	9.1E+00 AF066009.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9878	15587	23087	5.91	6.9E+00 BE671806.1	EST, HUMAN	BD1651038R1 NH_MGC_31 Homo sapiens cDNA clone IMAGE3934592.3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5848	15754	28571	1.71	8.7E-00	AB019788.1	NT	Cytopc pythogaster Cptb05 premature mRNA, partial cds
5848	15754	28572	1.71	8.7E-00	AB019788.1	NT	Cytopc pythogaster Cptb05 premature mRNA, partial cds
9343	10378	20159	1.76	8.4E-00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
7439	15452	28542	3.68	8.1E-00	AJ131719.1	NT	Zea mays mRNA for legumin-like protease (sec2a)
8509	18381		2.31	8.0E-00	P41820	SWISSPROT	BREIFELIN A RESISTANCE PROTEIN
6340	18209		2.07	7.8E-00	AL445085.1	NT	Thermoplasma acidophilum complete genome; segment 3/6
6958	16747	20540	1.53	7.5E-00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
6958	16747	20541	1.53	7.5E-00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5544	15460	28531	2.58	7.4E-00	BF700517.1	EST_HUMAN	602128976F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE4285506 5'
7085	15602	27155	3.83	7.4E-00	P04629	SWISSPROT	HISTIDINE RICH GLYCOPROTEIN PRECURSOR
7085	15602	27156	3.83	7.4E-00	P04629	SWISSPROT	HISTIDINE RICH GLYCOPROTEIN PRECURSOR
2947	12874	22671	4.2	7.2E-00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
2947	12874	22672	4.2	7.2E-00	L12051.1	NT	Lycopodium obscurum Mill. GTPase (SAR2) mRNA, complete cds
6239	16105	28254	1.45	6.9E-00	P34812.1	EST_HUMAN	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6239	16105	28255	1.3	7.1E-00	P28168	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7535	17388		9.48	7.1E-00	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
8590	16577	28590	3.26	7.1E-00	P05850	SWISSPROT	HYPOHETICAL 17.3 KDA PROTEIN IN URDA-PHASE INTERGENIC REGION
8575	17655	27593	2.88	7.0E-00	P46510	SWISSPROT	HYPOHETICAL 17.3 KDA PROTEIN IN URDA-PHASE INTERGENIC REGION
8818	16697	26580	2.72	6.9E-00	P32659	SWISSPROT	WD-40 REPEAT PROTEIN NS3
7505	17776	28018	1.3	6.9E-00	P14834	SWISSPROT	KOS RECOMBINANT PROTEIN L4(L2)
8874	15464	26580	1.45	6.8E-00	W03412.1	EST_HUMAN	DNA MISMATCH REPAIR PROTEIN MUTS
8874	15464	26581	1.45	6.8E-00	W03412.1	EST_HUMAN	2267671 r1 Soares melanocyte 206-M Homo sapiens cDNA clone IMAGE_267660 5'
7277	17154		1.47	6.8E-00	P46307	SWISSPROT	2267671 r1 Soares melanocyte 206-M Homo sapiens cDNA clone IMAGE_267660 5'
7683	17713	27957	3.82	6.8E-00	Q03570	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP6]
7795	17046	27851	2.1	6.6E-00	Q03570	SWISSPROT	HYPOHETICAL 157.0 KDA PROTEIN C98c10.5 IN CHROMOSOME III
7795	17046	27852	2.1	6.6E-00	Q03570	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
8471	18344		2.17	6.6E-00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C053.06C
7296	17172	27372	8.32	6.6E-00	Q03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP42; COAT PROTEIN GP46]
7616	17497		1.44	6.2E-00	A1010801.1	NT	Schizosaccharomyces pombe unknown mRNA
9528	15933	25556	7.16	5.9E-00	AF165142.1	NT	Mus musculus mixed lineage kinase 3 (Mlx3) and two pore domain K+ channel subunit (Kcnk9) genes, complete cds
3479	13395		0.91	5.9E-00	7691557	NT	Homo sapiens DESCI1 protein (DESCI1), mRNA

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8770	17919	28166	2.44	5.0E+00 Q15276	SWISSPROT	LYCOPENE BETA CYCLASE	
8759	17918	28165	2.65	5.9E+00 P11890	SWISSPROT	PEUPOLYSIN (THIO-ACTIVATED CYTOLYSIN)	
8697	18773		1.94	5.9E+00 AL161571.2	NT	Ankrapais thaliana DNA chromosome 4, contig fragment No. 67	
6593	16473		1.62	5.4E+00 C61092	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-IN; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]	
7759	17619	27646	1.44	5.4E+00 Q17064	SWISSPROT	RHODOPSIN	
7759	17619	27650	1.44	5.4E+00 Q17064	SWISSPROT	RHODOPSIN	
4875	14561	24354	1.54	5.3E+00 L43126.1	NT		
6710	16590		4.04	5.3E+00 P24205	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)	
6859	16708	29003	3.21	5.3E+00 Q27505	SWISSPROT	PROBABLE ANTIBACTERIAL PEPTIDE POLYPROTEIN PRECURSOR	
7555	17505	27730	1.21	5.1E+00 Q09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROBICIN N IMMUNITY PROTEIN)	
7559	17609	28030	3.06	5.0E+00 AF162445.2	NT	Genis familiaris skeletal muscle chloride channel (GCL-1) (GCLN1) mRNA, complete cds	
8610	18477	28748	10.93	5.0E+00 Z83890.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162	
3972	13879		9.43	4.9E+00 AF180293.1	NT	Emica australis histone H3 (H3) gene, partial cds	
6970	19547		5.01	4.9E+00 AW175067.1	EST_HUMAN	PAC-BT0547-310100-002-504 BT0547 Homo sapiens cDNA	
268	10251	20071	2.03	4.7E+00 BF240582.1	EST_HUMAN	80187654F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE-4089718 5'	
287	10251	20071	1.92	4.7E+00 BF240582.1	EST_HUMAN	80187654F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE-4089718 5'	
3259	13160	23698	4.01	4.7E+00 AL152365.2	NT	Homo sapiens chromosome 21, segment H521C080	
6576	16434	28517	1.48	4.6E+00 C71535.1	NT	Melanococcus leucon section 111 of 180 of the complete genome	
8881	18653	28686	1.98	4.5E+00 AC01044.1	NT	Archaeoglobus fulgidus section 03 of 172 of the complete genome	
3003	12591	22723	0.86	4.4E+00 BF1530893.1	EST_HUMAN	60207258F1 NCI CGAP_Eln67 Homo sapiens cDNA clone IMAGE-4215284 5'	
3003	12591	22724	0.86	4.4E+00 BF1530893.1	EST_HUMAN	60207258F1 NCI CGAP_Eln67 Homo sapiens cDNA clone IMAGE-4215284 5'	
5754	19571		1.85	4.4E+00 X13414.1	NT	Marine (gene for MHC class II(a) associated invariant chain	
6398	16298	26420	2.01	4.3E+00 Y13402.1	NT	Pharmodum talpaeum P2847v1 gene, exon 1	
8235	18116		7.49	4.3E+00 AF240785.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds	
5387	13306		2.82	4.2E+00 P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)	
6090	18043	26166	1.57	4.2E+00 P13883	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	
6090	18043	26167	1.57	4.2E+00 P13883	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)	
7182	17059	27249	5.45	4.2E+00 AB000103.1	EST_HUMAN	w67g63.x1 Boreas_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE-230092 3'	
6517	16376	29533	7.65	4.1E+00 Q23810	SWISSPROT	YY1 PROTEIN PRECURSOR	
6577	16435	29518	3.31	4.1E+00 P28654	SWISSPROT	GENE 68 PROTEIN	
6577	16435	29519	3.31	4.1E+00 P28654	SWISSPROT	GENE 68 PROTEIN	

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6817	16497	28884	2.95	4.1E+00 U67503.1	EST_HUMAN	NT	Pen triglycides novel repetitive sub LTR element in the RNU2 locus
7576	17427	27841	2.31	4.1E+00 BF62425.1	EST_HUMAN	NT	9022476291 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209.5
8259	18139	28977	2.89	4.1E+00 PQ8716	SWISSPROT	EST_HUMAN	HYPOTHETICAL PROTEIN HMLF1
8339	18218		12.46	4.1E+00 BE85880.1	EST_HUMAN	EST_HUMAN	80750701F NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3009051.5
9872	19231	25241	1.86	4.1E+00 P47878	SWISSPROT	SWISSPROT	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 (IGFBP-1) (IGF-BINDING PROTEIN 1)
6289	19131	26285	1.37	4.0E+00 Q330.0	SWISSPROT	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
8768	17917	28164	2.17	4.0E+00 P14546	SWISSPROT	SWISSPROT	CYTOCHROME C OXIDASE POLYPEPTIDE III
8635	18948	28034	3.34	4.0E+00 P07564	SWISSPROT	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E); NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5))
8835	18948	28035	3.34	4.0E+00 P07564	SWISSPROT	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E); NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5))
3459	13375	25181	3.89	3.9E+00 X64518.1	NT	NT	Human terminal vesicle secretory protein 92 (MSVSP92) gene, promoter region
4228	14124		0.99	3.9E+00 AF05496.1	EST_HUMAN	NT	Human terminal vesicle secretory protein 92 (MSVSP92) gene, promoter region
5471	15391	25454	2.47	3.9E+00 BE814387.1	EST_HUMAN	EST_HUMAN	MDR-BN0070-300050-028-H05 BN0070 Homo sapiens cDNA
5471	15391	25455	2.47	3.9E+00 BE814387.1	EST_HUMAN	EST_HUMAN	MDR-BN0070-300050-028-H05 BN0070 Homo sapiens cDNA
6108	19002	28140	4.46	3.9E+00 P39259	SWISSPROT	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RP8F INTERGENIC REGION
6355	19218	28379	4.09	3.9E+00 M23007.1	NT	NT	Human MHC class II lymphocyte antigen (DP-4-allele-1) gene, exon 2
6840	18719	28913	2.32	3.9E+00 X09505.1	NT	NT	Xenopus mRNA for M4 muscarinic receptor
8695	17879	28120	3.09	3.9E+00 Y18000.1	NT	NT	Homo sapiens NF2 gene
8715	18532	28916	5.58	3.9E+00 AA091489.1	EST_HUMAN	EST_HUMAN	trtBat2.51 NCL CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1189318 similar to gp-A10416
2598	12459		2.4	3.8E+00 AE001602.1	NT	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);
6911	19789	28882	1.19	3.8E+00 D44726.1	EST_HUMAN	EST_HUMAN	Helicobacter pylori, strain J99, section 123 of 132 of the complete genome
3038	13845	28622	10.09	3.7E+00 AL161539.2	NT	NT	HUMSLIPY195 Human brain cDNA Homo sapiens cDNA clone 148
8730	16595	28972	2.13	3.7E+00 BF686279.1	EST_HUMAN	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig, fragment Na_39
8730	16595	28973	2.13	3.7E+00 BF686279.1	EST_HUMAN	EST_HUMAN	902120551F NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4277748.5
876	10518	20322	2.1	3.6E+00 AV781055.1	EST_HUMAN	EST_HUMAN	902120551F NIH_MGC_50 Homo sapiens cDNA clone IMAGE:4277748.5
7022	18959	27090	3.69	3.6E+00 AE004447.1	NT	NT	AV781055 MSH Homo sapiens cDNA clone MDSB1E10.5
7022	18959	27091	3.69	3.6E+00 AE004447.1	NT	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome
7022	18959	27091	3.69	3.6E+00 AE004447.1	NT	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8228	18110		3.78	3.6E+00	M67056.1	NT	Escherichia coli glycerophosphate dehydrogenase (gpdH) gene, partial cds; and the translation start site has been verified (gpdH), the translation start site has been verified (gpdH), and repressor protein (gpdH) genes, complete cds
3209	13133	22634	1.04	3.6E+00	AF221538.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
1499	11400	21200	3.57	3.4E+00	AF254577.1	NT	Brassica napus RPB6d mRNA, complete cds
2532	12406	22286	1.02	3.4E+00	AL16378.2	NT	Homo sapiens chromosome 21 segment HS21C078
6354	16217	26378	2.41	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7889	17739	27692	3.17	3.4E+00	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
8818	18031	28919	1.82	3.4E+00	L77670.1	NT	Homo sapiens DICeocyte syndrome critical region, centromeric and
5036	14008	24679	1.41	3.3E+00	7682156	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
5036	14008	24680	1.41	3.3E+00	7682156	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
492	10435	20248	1.39	3.2E+00	X99422.1	NT	D. rerio zc-50 POU gene
3938	10435	20248	0.79	3.2E+00	X99422.1	NT	D. rerio zc-50 POU gene
5439	16359	25416	2.66	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE CYTOSOLIC
5439	16359	25416	2.66	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE CYTOSOLIC
5808	18713	28326	2.03	3.2E+00	P16931	SWISSPROT	NADH-LUBICQUONE OXIDOREDUCTASE CHAIN 4
5808	18713	28326	2.03	3.2E+00	P16931	SWISSPROT	NADH-LUBICQUONE OXIDOREDUCTASE CHAIN 4
6569	16421	26608	2.35	3.2E+00	Y13555.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps4, yps4, yps8, yps18 genes
6569	16421	26610	2.35	3.2E+00	Y13555.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps4, yps4, yps8 genes
7221	17098	27501	1.17	3.2E+00	P13061	NT	PERPLASMIC [NHE] HYDROGENASE SMALL SUBUNIT (NHE HYDROGENASE SMALL CHAIN)
7491	17361	27567	1.17	3.2E+00	Q10735	NT	Scorciae theonine deaminase (LTV) gene, complete cds
7637	17657	27652	1.69	3.2E+00	A030691.2	NT	Oryza sativa OsCDS gene for glutyl cyclase C, complete cds
9066	18683	25574	4.32	3.2E+00	Q13396.1	NT	Sua scrofa choline acetyltransferase gene, promoter region
5592	15467	25574	2.42	3.1E+00	Q10735	SWISSPROT	HYPOHETICAL 142.5 KD PROTEIN C25E202 IN CHROMOSOME 1
7000	16677	27067	4.35	3.1E+00	P46894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE1 I'DEIODINASE)(DIOI)(TYPE 1 DIOI)(DIOI)
7000	16677	27068	4.35	3.1E+00	P46894	SWISSPROT	TYPE 1 IODOTHYRONINE DEIODINASE (TYPE1 I'DEIODINASE)(DIOI)(TYPE 1 DIOI)(DIOI)
7334	17238		3.8	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMAD] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBUNIT 3C) (NR3C) (NMADRC)
7620	17770	28009	4.78	3.1E+00	P49365	SWISSPROT	DEOXYHYMINE SYNTHASE (DH5)
						SWISSPROT	GENOME POLYPYRUTIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN E (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS9))
8759	17908		3.78	3.1E+00	F35915	SWISSPROT	retinoic acid nuclear receptor isoform beta 2 [lncs, embryonal sarcoma cell line, PCCT-MZ1, mRNA, 2971 nt]
8774	16591		3.35	3.1E+00	S60980.1	NT	

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2607	12737	22535	1.06	3.0E+00	8923984	NT	Homo sapiens hypothetical protein PH00896 (PH00896), mRNA
6245	15156	24970	1.63	3.0E+00	X63006.1	NT	S. aureus genes encoding SaeB9 DNA methyltransferase and SaeB9 restriction endonuclease
9273	16111	9.5	3.0E+00	P18406	SWISSPROT		PROTEIN PRECURSOR (3CHr1)
7164	17041		1.46	3.0E+00	X67838.1	NT	B. napus DNA for myosinase
							RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2)
							(ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
8374	18251	28501	6.51	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2)
							(ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
8374	18251	28502	6.51	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2)
							(ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
1894	11898	21747	2.55	2.9E+00	AE020225.2	NT	Chlamydia pneumoniae AR39, section 53 of 54 of the complete genome
6129	15076	28112	1.63	2.9E+00	X26879.1	NT	F. pringlei adpA, gene for P-protein of the glycine cleavage system
6392	16146	28300	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
6392	16146	28301	4.47	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
8410	16271	28433	5.19	2.9E+00	P146589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
1441	11349	21212	6.79	2.9E+00	AF168398.1	NT	Bovine brucella mltA, K (mliK) gene, partial cds, chloroplast gene for chloroplast product
1615	11518		3.12	2.9E+00	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
6325	16188	28390	4.78	2.9E+00	8383724	NT	Mus musculus endonucrin (LOC55423), mRNA
230	10195	20012	4.63	2.7E+00	6679303	NT	Mus musculus per-haemol repeat gene 3 (Phc3), mRNA
5408	15327	25377	1.75	2.7E+00	6679303	NT	Mus musculus per-haemol repeat gene 3 (Phc3), mRNA
7185	17062		2.21	2.7E+00	L14005.1	NT	Homo sapiens apoa polyomorphism Kappa IV gene, exons 1 and 2
7998	17846	24253	2.16	2.7E+00	BE063827.1	NT	Bovine chaperonin 14 cDNA library under conditions of nitrogen deprivation
4578	14467		4.35	2.6E+00	AF068746.1	NT	CH0410281-03159-067404 B10281 Homo sapiens cDNA
5405	15324	25373	1.97	2.6E+00	6755607	NT	Mus musculus springtime kinase (SPHK1b) mRNA, complete cds
5405	15324	25374	1.97	2.6E+00	6755607	NT	Mus musculus SRY-box containing gene 13 (Sbx13), mRNA
							Mus musculus SRY-box containing gene 13 (Sbx13), mRNA
6633	16391		5.42	2.6E+00	AF255002.1	NT	Mus musculus S12-containing isolectin 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
6636	16576	26767	1.2	2.6E+00	AJ132180.1	NT	Felis leo necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
8635	16579	26768	1.2	2.6E+00	AJ132180.1	NT	Felis leo necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
7697	17418	27634	2.55	2.6E+00	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
7697	17417		1.52	2.6E+00	5056193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
							Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
9711	19049		2.31	2.6E+00	11419220	NT	Homo sapiens ATP-binding domain, sub-family B (ADRF1AP), member 4 (ABCR4), mRNA
1448	11353	21216	2.08	2.6E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1448	11353	21217	2.08	2.5E+00 AJ271844.1	NT		Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
6562	15498	28537	2.33	2.5E+00 P13485	SWISSPROT		TECHOIC ACID BIOSYNTHESIS PROTEIN F
5552	15498	28538	2.33	2.5E+00 P13485	SWISSPROT		TECHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15498	28537	1.71	2.5E+00 P13485	SWISSPROT		TECHOIC ACID BIOSYNTHESIS PROTEIN F
5886	15498	28538	1.71	2.5E+00 P13485	SWISSPROT		TECHOIC ACID BIOSYNTHESIS PROTEIN F
6661	16419	28568	1.34	2.5E+00 AW949158.1	EST_HUMAN		QV4-FT0065-10560-205-p07 FT0065 Homo sapiens cDNA
7264	17141	27334	1.75	2.5E+00 D63007.1	NT		Rice DNA for address C-1, complete cds
6059	18931		2.25	2.5E+00 AF239665.1	NT		Mus musculus E1H4-F1 gene, partial cds; and ELN gene, partial cds
2680	12907	22707	0.86	2.4E+00 M24232.1	NT		Chicken alpha-3 collagen type VI mRNA, 3' end
4819	14699	24485	7.62	2.4E+00 P02843	SWISSPROT		Homo sapiens double C2-like domain, alpha (DOC2A) mRNA
5657	15699	25694	4.19	2.4E+00 P23842	SWISSPROT		VITELLOGENIN PRECURSOR (YOLK PROTEIN 1)
6733	16913	28902	2.14	2.4E+00 P23842	SWISSPROT		CD21 RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD21) (T14)
6733	16913	28903	2.14	2.4E+00 P23842	SWISSPROT		CD21 RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD21) (T14)
6769	16939		2.63	2.4E+00 AE001486.1	NT		Helicobacter pylori strain J99 section 47 of 132 of the complete genome
7029	16903		1.71	2.4E+00 AW15126.1	EST_HUMAN		BC2-PT004-021392-011-005 PT0004 Homo sapiens cDNA
7125	17002	27194	9.46	2.4E+00 P24091	SWISSPROT		ENDOCHITINASE B PRECURSOR (CHN-B)
7771	17921	27583	2.5	2.4E+00 P13673	SWISSPROT		SKIN GRANULE PROTEIN PRECURSOR
7771	17921	27584	2.5	2.4E+00 P13673	SWISSPROT		SKIN GRANULE PROTEIN PRECURSOR
7820	17970	27911	2.18	2.4E+00 X62511.1	NT		Hepatitis CTGF gene and promoter region
7851	17731		8.49	2.4E+00 P06689	SWISSPROT		XYLOGLUCANINASE (XYLOGLUCINASE)
7814	17764	28002	1.67	2.4E+00 BE325702.1	EST_HUMAN		h6306.x1 NCL CGAP K6H1 Homo sapiens cDNA clone IMAGE:3133187 3'
7814	17764	28003	1.67	2.4E+00 BE325702.1	EST_HUMAN		h6306.x1 NCL CGAP K6H1 Homo sapiens cDNA clone IMAGE:3133187 3'
8428	18302	28568	1.77	2.4E+00 Y14079.1	NT		Bacillus subtilis chromosomal DNA, region 76 degrees: glpPHD operon and downstream
8665	18554	28839	2.52	2.4E+00 AF159652.2	NT		Frugilula xanthisma cytochrome oxidase (ApoSC) gene, ApoSC-α allele, complete cds
1233	11140	28992	0.36	2.3E+00 Z46724.1	NT		G domesticus artificial single chain antibody gene (L3)
4031	16293		1.28	2.3E+00 AJ407081.1	NT		Bos taurus pituitary gene for cytochrome b
5408	13034	25431	2.22	2.3E+00 6978654	NT		Rattus norvegicus ATPase, Cxx+ transposon, ubiquitous (Atp2a3), mRNA
6479	10755		2.3	2.3E+00 P07169	SWISSPROT		MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
6573	10431	20613	1.53	2.3E+00 NC02055.1	NT		Minisat DnaK and dnaJ genes homologues coding for DnaK and DnaJ
7280	17165	27264	1.81	2.3E+00 Q11127	SWISSPROT		ALPHA-1,3-FUCOSYL TRANSFERASE (GALACTOSIDE 3,4-L-FUCOSYL TRANSFERASE)
8088	18793	28083	2.6	2.3E+00 BF541067.1	EST_HUMAN		902069121F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4088173 5'
8088	18793	28084	2.6	2.3E+00 BF541067.1	EST_HUMAN		902069121F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:4088173 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9304	19002	28333		4	2.3E+00	EST_HUMAN	001433673f1 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:3918943 5'
9936	19405		1.97	2.3E+00	AF281892.1	NT	Neurospora crassa G protein alpha subunit GNA-3 (gna-3) gene, complete cds
4216	14114	23891	3.82	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
4216	14114	23892	3.82	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
5276	15168	24973	10.08	2.2E+00	O68307	SWISSPROT	SORTILIN-RELATED RECEPTOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY UPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) >
5276	15168	24974	10.08	2.2E+00	O68307	SWISSPROT	SORTILIN-RELATED RECEPTOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY UPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) >
5926	18505	28707	9.09	2.2E+00	BE250383.1	EST_HUMAN	009434911 NH1_MGC_17 Homo sapiens cDNA clone IMAGE:2846777 3'
5935	18741	28653	3.3	2.2E+00	O03335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU2
5978	18923	20066	2.89	2.2E+00	P07149	SWISSPROT	INSULIN-LIKE GROWTH FACTOR I PRECURSOR (IGF-I) (SOMATOMEDIN A)
6155	18113		3.14	2.2E+00	A4594574.1	EST_HUMAN	y89602.01 NCI_CGAP_C070 Homo sapiens cDNA clone IMAGE:1068370 3'
9460	16344	26874	51.58	2.2E+00	A4446012.1	EST_HUMAN	y89610.01 Soares, total, fetus, N29-F8, 9m Homo sapiens cDNA clone IMAGE:76934 5'
7351	17250		11.83	2.2E+00	BE741878.1	EST_HUMAN	001694735f1 NH1_MGC_9 Homo sapiens cDNA clone IMAGE:394861 5'
7318	19468		2.1	2.2E+00	O34705	SWISSPROT	TRANSFERRIN TYROSINE PROTEIN A
7763	17653	27606	1.56	2.2E+00	A1260373.1	EST_HUMAN	q16063.x1 Soares, placenta, 2NHPR/86H1 Homo sapiens cDNA clone IMAGE:1639066 3'
7763	17653	27606	1.56	2.2E+00	A1260373.1	EST_HUMAN	q16063.x1 Soares, placenta, 2NHPR/86H1 Homo sapiens cDNA clone IMAGE:1639066 3'
7812	17662	27502	2.28	2.2E+00	BF246782.1	EST_HUMAN	similar to gb:100483 GLUTATHIONE PEROXIDASE (HUMAN);
7975	17828	28066	2.88	2.2E+00	AF183416.1	NT	001865981f1 NH1_MGC_57 Homo sapiens cDNA clone IMAGE:4075951 5'
8739	17898	28132	4.5	2.2E+00	P07011	SWISSPROT	HOMO sapiens ovarian granulosa cell T3.0 lida protein HGR74 homolog mRNA, complete cds
8968	17900	28665	4.67	2.2E+00	P10407	SWISSPROT	URONODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
557	12870	20304	6.81	2.1E+00	AF132012.2	NT	EARLY E1A 28 KD PROTEIN
3839	13455		1.19	2.1E+00	AW449866.1	EST_HUMAN	Mus musculus pre-T cell receptor alpha gene, enhancer' region and upstream region
6074	16057	26206	3.72	2.1E+00	O70159	SWISSPROT	UPLH-A-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
6195	16955	26087	4.7	2.1E+00	N28375.1	EST_HUMAN	y48810.01 Soares, melanocyte 2b6m Homo sapiens cDNA clone IMAGE:270618 5' similar to gb:M55964
6948	18263		1.59	2.1E+00	AI123630.1	EST_HUMAN	YF8810.01 Soares, melanocyte 2b6m Homo sapiens cDNA clone IMAGE:2744550 3'
1178	11089	20634	1.23	2.0E+00	AF186527.1	NT	AU123630.01 FR42 Homo sapiens cDNA clone NT25V/2008971 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1178	11089	26935	1.23	2.0E+00	AF16527.1	NT	Homo sapiens p22bDdel (DOKDEL) mRNA, complete cds
1313	11219	21078	1.43	2.0E+00	AF204927.1	NT	Oryzias latipes Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
1557	11462	26752	3.13	2.0E+00	P29582	SWISSPROT	PUTATIVE IRINA METHYLTRANSFERASE SPB1
2102	11991	21800	4.6	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
2102	11991	21801	4.6	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4011	13917	23652	2.09	2.0E+00	AW664496.1	EST HUMAN	h13d6.5X1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gp2X01677
4011	13917	23653	2.09	2.0E+00	AW664496.1	EST HUMAN	h13d6.5X1 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gp2X01677
6678	15558	26751	3.8	2.0E+00	AB008676.1	NT	Escherichia coli O157 DNA, map position at 45 min, complete cds
6678	15558	26752	3.8	2.0E+00	AB008676.1	NT	Escherichia coli O157 DNA, map position at 45 min, complete cds
6678	15558	26753	3.8	2.0E+00	AB008676.1	NT	Escherichia coli O157 DNA, map position at 45 min, complete cds
7170	17047	27237	3.3	2.0E+00	F31500.1	EST HUMAN	HSPD2703 HNS Homo sapiens cDNA clone #4000117808
9529	18613	26986	5.81	2.0E+00	5834443	NT	Gallus gallus mitochondrion, complete genome
5437	15357	26412	4.67	1.9E+00	6754336	NT	Mus musculus insulin 1, 4,5-epithelial receptor 1 (Ibr1), mRNA
5437	15357	26413	4.67	1.9E+00	6754336	NT	Mus musculus insulin 1, 4,5-epithelial receptor 1 (Ibr1), mRNA
6047	15950	26413	2.27	1.9E+00	G63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN R44
6027	15863	26939	2.58	1.9E+00	P02437	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
6027	15863	27000	2.58	1.9E+00	P02437	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
7032	15809		3.38	1.9E+00	BF360206.1	EST HUMAN	CAC4MT011470003025412MT0114 Homo sapiens cDNA
7158	17033		1.95	1.9E+00	051781	SWISSPROT	ARGININE DEIMINASE (AD) (ARGININE DITHIOYLASE) (AD)
3054	12981	22775	1.71	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3082	13009	22799	4.49	1.8E+00	U04356.1	NT	Synedrochoc sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (epsilon) genes, complete cds
3082	13009	22800	4.49	1.8E+00	U04356.1	NT	Synedrochoc sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (epsilon) genes, complete cds
5577	15482		2.22	1.8E+00	F16502	EST HUMAN	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
5712	15920	26723	1.9	1.8E+00	BF31099.1	SWISSPROT	h01897854F1 NIH MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6043	15916	26078	1.3	1.8E+00	BF308592.1	EST HUMAN	h01897854F1 NIH MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7140	17017	27210	2.09	1.8E+00	Q43821	SWISSPROT	EMBRYONAL FYN ASSOCIATED SUBSTRATE (HEFS)
7293	17769	27369	1.21	1.8E+00	R31042.1	EST HUMAN	h172d08.1 Soares placenta N8dHP Homo sapiens cDNA clone IMAGE:135276 5'
7599	17149		3.29	1.8E+00	AF111849.1	NT	Homo sapiens FROU303 mRNA, complete cds
8938	18301		3.79	1.8E+00	P39052	SWISSPROT	HYPOTHETICAL 75.5 KD PROTEIN IN SCH-CHIMY3 INTERGENIC REGION

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HR BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6428	18934		4.01	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
5904	19119		2.4	1.8E+00	5906404	NT	Rattus norvegicus Acin-1-related protein complex 1b (Acp1b), mRNA
5968	19429		1.34	1.8E+00	BF13806.1	EST_HUMAN	R016030907 NIH_MGC, 18 Homo sapiens cDNA clone IMAGE:4135898 5'
1092	11008	20849	1.92	1.7E+00	Q00114	SWISSPROT	LEVANSUGRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
2225	12110	22013	3.25	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2321	12202	22101	1.02	1.7E+00	AI141067.1	EST_HUMAN	ca26H05.41 Soares, NIH/MPRI, S1 Homo sapiens cDNA clone IMAGE:1767137 3'
4556	14232	24037	0.84	1.7E+00	Q00114	SWISSPROT	LEVANSUGRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
5448	15339	24244	1.48	1.7E+00	BE003564.1	EST_HUMAN	Q04210282-171256-127-405 BT0282 Homo sapiens cDNA
5445	15369	25425	1.48	1.7E+00	BE003564.1	EST_HUMAN	Q04210282-171256-127-405 BT0282 Homo sapiens cDNA
5984	15575	25873	3.58	1.7E+00	G01718	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1)
7014	15991		1.29	1.7E+00	BF30000.1	EST_HUMAN	R016042587 NIH_MGC, 17 Homo sapiens cDNA clone IMAGE:4140084 5'
7282	18467	27355	2.18	1.7E+00	Q04479	SWISSPROT	HOMEOBOX PROTEIN DLX3
7282	18467	27355	2.18	1.7E+00	Q04479	SWISSPROT	HOMEOBOX PROTEIN DLX3
8874	18886	28977	1.78	1.7E+00	W22424.1	EST_HUMAN	37637 Human retina cDNA, Top5034 cleaved sublibrary Homo sapiens cDNA not directional
8984	19044		1.37	1.7E+00	AF167943.1	EST_HUMAN	h23407.4 NO1 CGAP, Gen4 Homo sapiens cDNA clone IMAGE:2287548 3' similar to contains MSRL11
9860	19351	25165	2.28	1.7E+00	AF168573.1	EST_HUMAN	g93001.41 Soares, Tellez, NHT Homo sapiens cDNA clone IMAGE:1793477 3' similar to contains L141 L1
1593	11832	21775	16.73	1.5E+00	AF168399.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
1997	11891	21763	3.61	1.5E+00	AF077374.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2003	11896	21768	1.66	1.6E+00	Y11344.1	NT	Mus musculus ST165N/Celli gene, exon 2
2238	12122		1.45	1.6E+00	X68373.1	NT	B. napus gene encoding endo-polygalacturonase
2631	12658	22668	2.62	1.6E+00	W59426.1	EST_HUMAN	h23901.14 Soares, Tellez, NHT, NHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
3645	13854		5.14	1.6E+00	BF970077.1	EST_HUMAN	g902800.11 NIH_MGC, 45 Homo sapiens cDNA clone IMAGE:4310591 3'
4295	14154	23028	1.44	1.6E+00	AF158827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SNARCA) mRNA, complete cds
4295	14154	23028	1.44	1.6E+00	AF158827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SNARCA) mRNA, complete cds
5018	14990	24057	3.14	1.6E+00	Y11344.1	NT	Mus musculus ST165N/Celli gene, exon 2
5018	14990	24057	3.14	1.6E+00	Y11344.1	NT	Mus musculus ST165N/Celli gene, exon 2
5559	15474	25549	2.19	1.6E+00	LD4808.1	NT	Brechidiano renio MHC class II DA-beta-201 gene, 3' end
6293	16190	26317	2.64	1.6E+00	BE097297.1	EST_HUMAN	RC0-CT0415-200700-432-c10 CT0415 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Exon Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6991	10591		1.21	1.6E-00	Q46378	SWISSPROT	VIRULENCE FACTOR IWIN HOMOLOG
6991	10700	29658	3.96	1.6E-00	AJ297131.1	NT	Mus musculus SIL MAP 17, CYP_a, SCL & CYP_b genes
7444	19465	29646	1.3	1.6E-00	A29246.1	NT	Mus musculus COL3A1 gene for collagen alpha-1(I) chain
7444	19465	29647	1.3	1.6E-00	X62046.1	NT	Mus musculus COL3A1 gene for collagen alpha-1(I) chain
7611	17462	27679	1.29	1.6E-00	T41290.1	EST_HUMAN	phb5c_191TV Outward Aluprimed IncDNA library Homo sapiens cDNA clone phb5c_191TV
7852	17702	27946	1.25	1.6E-00	AW835644.1	EST_HUMAN	QV41.T0016-090200-100-307 T0016 Homo sapiens cDNA
8217	15520	25601	6.69	1.6E-00	AF025931.1	NT	Homo sapiens transglutaminase type 1 (Tgase1) gene, promoter region
8944	18752	29047	3.25	1.6E-00	AF104313.1	NT	Homo sapiens unknown mRNA
9602	16379		1.65	1.6E-00	AF176403.1	EST_HUMAN	AV764033 MDS Homo sapiens cDNA clone MDS4H08.5
30	10017	19812	4.29	1.6E-00	U53449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jp2-2) mRNA, complete cds
231	10200	20014	1.76	1.5E-00	AE02201.2	NT	Chlamydomonas reinhardtii pntA39, section 32 of 84 of the complete genome
605	10541		1.79	1.5E-00	6752961	NT	Mus musculus alpha 2(I) globulin, complete genome
2359	12239	22135	2.46	1.5E-00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2498	12344	22237	2.02	1.5E-00	6576350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tlimt1), mRNA
3369	12239	22193	2.22	1.5E-00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3329	13249	23054	0.62	1.5E-00	AJ131405.1	NT	Dendroica auduboni RT, section 82 of 225 of the complete chromosome 1
8955	19762	25860	2.71	1.5E-00	R17676.1	EST_HUMAN	y910622.11 Some refines N26-4HR Homo sapiens cDNA clone IMAGE:31865.5
6250	16069	26208	1.42	1.5E-00	BE763396.1	EST_HUMAN	HYPOPHYSICAL 118.4 KD PROTEIN IN BAT 2-DALS INTERGENIC REGION PRECURSOR
6250	16116	26208	29.13	1.5E-00	F47779	SWISSPROT	HYPOPHYSICAL 118.4 KD PROTEIN IN BAT 2-DALS INTERGENIC REGION PRECURSOR
7571	17921	27747	7.96	1.5E-00	BF370754.1	EST_HUMAN	RG2-TN0078-15000-004-005 TN0078 Homo sapiens cDNA
7752	17632		1.71	1.5E-00	BF337944.1	EST_HUMAN	602035771F1 NGL CGAP Brn64 Homo sapiens cDNA clone IMAGE:418866.5
7856	17706	27951	1.96	1.5E-00	AA077699.1	EST_HUMAN	263606.61 Some refines N26-4HR Homo sapiens cDNA clone IMAGE:381306.5
7856	17706	27952	1.96	1.5E-00	AA077699.1	EST_HUMAN	263606.61 Some refines N26-4HR Homo sapiens cDNA clone IMAGE:381306.5
8702	18520	28802	3.91	1.5E-00	AL134197.1	EST_HUMAN	DKFZP595M0122 protein (DKFZP595M0122), mRNA
8828	18641		10.73	1.5E-00	XL7380.1	NT	DKFZP595M0122 protein (DKFZP595M0122), mRNA
9223	18646		1.5	1.5E-00	6753287	NT	Mus musculus caspase 8 associated protein 2 (Casp8ag2), mRNA
9596	19178		2.89	1.5E-00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
9590	19243		1.42	1.5E-00	6978462	NT	Thermoplasma acidophilum complete genome, segment 3/5
27	10014	19808	1.28	1.4E-00	7691685	NT	Fallus norvegicus 5 - Lipoxigenase (Alu6), mRNA
27	10014	19809	1.28	1.4E-00	7691685	NT	Homo sapiens DKFZP595M0122 protein (DKFZP595M0122), mRNA
2231	12116		0.95	1.4E-00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (gluA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2286	12169		9.38	1.4E+00	U67922.1	NT	Osteonin protein gene, complete cds
2634	12501	22394	1.63	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2746	12808	22600	3.29	1.4E+00	AF064564.2	NT	Fugu ribotypes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WBS1 protein (WBS1) genes, complete cds
2746	12808	22501	3.29	1.4E+00	AF064564.2	NT	Fugu ribotypes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WBS1 protein (WBS1) genes, complete cds
3034	12962	22755	1.01	1.4E+00	AED02324.2	NT	Chlamydia muridarum, section 65 of 65 of the complete genome
3034	12962	22756	1.01	1.4E+00	AED02324.2	NT	Chlamydia muridarum, section 65 of 65 of the complete genome
3297	13213		0.87	1.4E+00	5453733	NT	Human sapiens MafK homolog (MAD2) mRNA
4162	14092	22835	1.09	1.4E+00	AW600455.1	EST_HUMAN	CAC0-NNT005-140300-285-100 NNT005 Homo sapiens cDNA
4162	14092	22836	1.09	1.4E+00	AW600455.1	EST_HUMAN	CAC0-NNT005-140300-285-100 NNT005 Homo sapiens cDNA
4482	14376	22839	1.63	1.4E+00	BF881647.1	EST_HUMAN	9921668971 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287565 5'
6137	15204		0.8	1.4E+00	Q07869	SWISSPROT	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5901	15313	22026	1.81	1.4E+00	AW054978.1	EST_HUMAN	W45597 c1 NGL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2810480 3'
5904	15313		5.17	1.4E+00	AB035363.1	NT	Homo sapiens mRNA for KIAA1167 protein, partial cds
6769	15702	26812	2.39	1.4E+00	C13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
5902	15785		4.9	1.4E+00	AB020971.2	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
5900	15790	26884	2.71	1.4E+00	Q52777	SWISSPROT	SYNAPSIN II
5900	15795	26885	2.71	1.4E+00	Q52777	SWISSPROT	SYNAPSIN II
6518	16181	26341	1.86	1.4E+00	AJ13269.1	NT	Homo sapiens cdcw11-1/2 locus, Contig1, D1S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7107	16984		5.21	1.4E+00	AJ27735.1	NT	Homo sapiens Xq pseudautosomal region; segment 12
7256	17133	27326	1.88	1.4E+00	B20486.1	EST_HUMAN	9538721 Scores Infant brain NIH Homo sapiens cDNA clone IMAGE:34545 5'
7303	17179	27391	3.37	1.4E+00	BE064697.1	EST_HUMAN	RC1-B10313-301200-012-05 B10313 Homo sapiens cDNA
8420	18234	28648	1.94	1.4E+00	AA195628.1	EST_HUMAN	260609.1 Scores, NIH/NIH_51 Homo sapiens cDNA clone IMAGE:669512 5' similar to contains element
8559	19426	29395	4.97	1.4E+00	AB000662.1	NT	HERF2 repetitive element
8709	19526	29808	5.15	1.4E+00	BE962107.2	EST_HUMAN	Homo sapiens APOC500 mRNA for APOE-1, complete cds
8709	19526	29809	5.15	1.4E+00	BE962107.2	EST_HUMAN	Homo sapiens APOC500 mRNA for APOE-1, complete cds
8727	19553	29957	2.66	1.4E+00	U30790.1	NT	Pharmococytic cerin 1, sp. ratti guanine nucleotide binding protein alpha subunit (pgc1) gene, complete cds
8727	19553	29958	2.66	1.4E+00	U30790.1	NT	Pharmococytic cerin 1, sp. ratti guanine nucleotide binding protein alpha subunit (pgc1) gene, complete cds
9221	19604		1.34	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
658	10498		1.67	1.3E+00	Z75840.1	NT	Mitochondrion gene encoding 4-Dihydroxyethyl-lysinate dehydrogenase
884	10810	20659	2.74	1.3E+00	AJ271192.1	NT	Cantharidin sp. partial 28S rRNA gene, isolate T10el
1113	11028		16.5	1.3E+00	Y18213.1	NT	Homo sapiens putative ribosomal RNA pseudogene for hair keratin, exons 2 to 7
1275	11183	21033	10.9	1.3E+00	4507986	NT	Homo sapiens zinc finger protein 157 (ZF222) (ZF157) mRNA
1276	11183	21034	10.8	1.3E+00	4507986	NT	Homo sapiens zinc finger protein 157 (ZF222) (ZF157) mRNA
1334	11241		1.62	1.3E+00	U61730.2	NT	Cdk1 isozyme p34 cyclin-dependent kinase 2 (cdk2) gene, complete cds
1593	11497		2.09	1.3E+00	AE02338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2190	12033		2.1	1.3E+00	ABG30447.1	NT	Cyprinid carp MRP3 and MASP3 genes for mannose-binding lectin-associated serine protease (MASP)
2303	12379		2.19	1.3E+00	BE690735.2	EST_HUMAN	301097123R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2309	12835	22632	1.12	1.3E+00		NT	Mus musculus alpha-spectrin 1, erythrocyte (Spn1), mRNA
3547	13463	23058	1.03	1.3E+00	AF016404.1	NT	Mus musculus alpha-spectrin 1, erythrocyte (Spn1), mRNA
4502	12835	22632	0.82	1.3E+00		NT	Mus musculus alpha-spectrin 1, erythrocyte (Spn1), mRNA
4504	14839	24607	0.98	1.3E+00	AJ25087.1	NT	Plasmodium relictum partial 83/AMA-1 gene for apical membrane antigen 1
4984	14839	24609	0.98	1.3E+00	AJ25087.1	NT	Plasmodium relictum partial 83/AMA-1 gene for apical membrane antigen 1
5065	15378	25874	7.78	1.3E+00	AN352834.1	EST_HUMAN	PMA-GT0285-291189-501-618 CT02851 Homo sapiens cDNA
5065	15378	25874	7.78	1.3E+00	AN352834.1	EST_HUMAN	PMA-GT0285-291189-501-618 CT02851 Homo sapiens cDNA
5854	15378	25874	7.78	1.3E+00	AN352834.1	EST_HUMAN	PMA-GT0285-291189-501-618 CT02851 Homo sapiens cDNA
6828	16707	26501	1.33	1.3E+00	M33466.1	NT	Stenotaphrum secundatum
6917	16795	26588	3.05	1.3E+00	BE95370.2	EST_HUMAN	Ornithine decarboxylase (ODC) gene product, complete cds
7054	16931		1.55	1.3E+00	9010247	NT	Stenotaphrum secundatum
7460	17350		5.44	1.3E+00	AF042084.1	NT	Homo sapiens GL004 protein (GL004), mRNA
7467	17357	27590	2.31	1.3E+00	X72019.1	NT	Homo sapiens heparan glucosaminyl 1,4-deacetylaseN sulfotransferase-2 gene, complete cds
7487	17357	27591	2.31	1.3E+00	X72019.1	NT	S alpha pH-1 mRNA for phosphatase
7574	17425	27639	1.45	1.3E+00	000764	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID
7620	17471	27650	1.27	1.3E+00	AI027028.1	EST_HUMAN	LYSOSOMAL ALPHA-MANNOSIDASE (LAMAN)
7675	17525	27751	4.9	1.3E+00	BE963379.2	EST_HUMAN	weh507.x1 NC1_OGAP_K011 Homo sapiens cDNA clone IMAGE:2482100 3'
7860	17710	27801	1.71	1.3E+00	AE004392.1	NT	601057110T NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3606195 3'
7874	17724	27808	1.39	1.3E+00	M25663.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
8078	17959		4.3	1.3E+00	Q14117	SWISSPROT	Campylobacter jejuni karumycin phosphotransferase (acpA-7) gene, complete cds
8271	18157	28398	2.34	1.3E+00	P25299	SWISSPROT	DHFRDOPYRIMIDINASE (DHFRASE) (HYDANTOINASE) (DHP)
							MENA 3'-END PROCESSING PROTEIN RNA15

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8299	18178	28424	2.23	1.3E+00	T18952.2	NT	Mus musculus desmin gene
8946	18510		1.81	1.3E+00	AW27479.1	EST HUMAN	xp0063.1 NC1 CGAP HN6 Homo sapiens cDNA clone IMAGE:2788083 3'
8926	18539	26923	2.82	1.3E+00	DA2042.1	NT	Human mRNA for KIAA0085 gene, partial cds
8995	18705	28969	2.71	1.3E+00	Z68692.1	NT	Sacchara subtilis genomic DNA 23.6k8 fragment
9392	19033		2.35	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel KIR2.2 (KCNJ12) gene, complete cds
9533	19139	25283	3.24	1.3E+00	BF348043.1	EST HUMAN	90202185FT NC1 CGAP Bms7 Homo sapiens cDNA clone IMAGE:4158452 5'
9544	19499		2.69	1.3E+00	P33444	SWISSPROT	ET GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
934	10571	20384	8.14	1.2E+00	AA476246.1	EST HUMAN	2122008 s1 Soares, fetal liver, spleen, INF5, 51 Homo sapiens cDNA clone IMAGE:431835 3'
805	10735	20578	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
808	10735	20579	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
809	10735	20580	1.33	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
860	10766		2.19	1.2E+00	P05228	NT	Homo sapiens hypodermal protein PRO3307 (PRO3307), mRNA
1145	11059	20901	5.53	1.2E+00	AF059242.2	NT	Elasid, elafin, serine/threonine synthase mRNA, complete cds
1187	11097	20943	1.77	1.2E+00	AF059242.2	NT	sea seed-borne mosaic virus complete genome
1187	11097	20944	1.77	1.2E+00	AF059242.1	NT	sea seed-borne mosaic virus complete genome
1093	11587	21746	1.05	1.2E+00	AF04052.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
3072	12999	22769	0.95	1.2E+00	AF020651.1	NT	Human sapiens mRNA for KIAA0874 protein, partial cds
3128	13053	22851	5.47	1.2E+00	AL161953.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3128	13053	22852	5.47	1.2E+00	AL161953.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3249	13172		2.9	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3311	13232	23038	0.78	1.2E+00	AF188740.1	NT	Homo sapiens LH33 gene, intron 2
3312	13233		0.69	1.2E+00	M81776.1	NT	Gallus T-cofactor mRNA, complete cds
3950	13564	23330	7.28	1.2E+00	U76902.1	NT	Mus musculus subunit-like serine protease LPC (P07) gene, exons 1 to 8, partial cds
3904	13814	23568	1.49	1.2E+00	BF373570.1	EST HUMAN	MRP-H7017-003900-203-g00_1 F01768 Homo sapiens cDNA
4201	13232	23038	1.09	1.2E+00	AF188740.1	NT	Homo sapiens LH33 gene, intron 2
4298	14166	23981	1.39	1.2E+00		NT	Homo sapiens LH33 gene, intron 2
4371	14267		1.84	1.2E+00	M87080.1	NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glr2), mRNA
4422	14316	24102	1.29	1.2E+00	AL161953.2	NT	Rattus norvegicus Glycine receptor alpha 2 subunit (glycine receptor, neonatal) (Glr2), mRNA
4460	14354	24145	1.82	1.2E+00	AF150495.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4485	14379	24145	5.44	1.2E+00	Y09200.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4884	13233		0.94	1.2E+00	M81776.1	NT	T. parvulus chloroplast rbcL gene, partial
5404	15329	25379	1.95	1.2E+00	AW1813276.1	EST HUMAN	G. gallus T-cofactor mRNA, complete cds
5738	15947	25753	2.47	1.2E+00	X74485.1	NT	MRP-S70191-140203-015-c05 ST0161 Homo sapiens cDNA
5765	15976	25753	3.28	1.2E+00	BE003113.1	EST HUMAN	D. hydei avyl repeat cluster DNA, fragment D
							QV44-BN0580-270400-189-403 UN0090 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5765	15704	25815	1.87	1.2E+00	X89094.1	NT	C-glutinin pta gene and acta gene
5768	15704	25816	1.87	1.2E+00	X89094.1	NT	C-glutinin pta gene and acta gene
5823	15729	25841	32.83	1.2E+00	AA75254.1	EST HUMAN	adAg12.51 Scores_NHT Homo sapiens cDNA clone 132374.3
5918	15823	25949	1.82	1.2E+00	AF181327.1	EST HUMAN	MF3-510161-140200-318-c05 S10161 Homo sapiens cDNA
6139	15986	26021	2.05	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
6365	16463	26352	1.9	1.2E+00	AV734585.1	EST HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAH03 5'
6503	16367	26544	2.4	1.2E+00	X74207.1	NT	Lactid pvd and pvf genes
6594	15951	27055	3.45	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
7218	17095	27265	1.74	1.2E+00	AW377210.1	EST HUMAN	MR2-01222-201098-001-407 G10222 Homo sapiens cDNA
7407	17274	27480	3.08	1.2E+00	X23830.1	NT	R communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
7540	17391	27601	1.8	1.2E+00	D11745.1	EST HUMAN	HUMH01A01 Liver HepG2 cell line, Homo sapiens cDNA clone hmo1.601
7711	17561	27706	3.28	1.2E+00	X59832.1	NT	H sapiens ENO3 gene for muscle specific enolase
8553	18442	28236	2.03	1.2E+00	AW1817617.1	EST HUMAN	PMA-010264-18158-007-481 ST02384 Homo sapiens cDNA
8559	18576	28236	23.47	1.2E+00	BE15791.1	EST HUMAN	PMA-010264-180300-007-410 HT0422 Homo sapiens cDNA
8722	17901	28145	4.87	1.2E+00	U50174.7	NT	Saltus nematodus synapsin-related protein 102 mRNA, complete cds
9114	18877	28787	2.3	1.2E+00	AF065398.1	NT	Mus musculus 90120 ribonucleoprotein SSKA10 gene, complete cds
9530	19572	29567	15.4	1.2E+00	AL165203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9549	19025	29567	1.49	1.2E+00	AF001815.1	NT	Bacillus halodurans genomic DNA, section 9/14
456	10400	20277	1.13	1.1E+00	D06690.1	NT	Human mRNA for KIAA0227 gene, partial cds
1728	11627	21496	1.39	1.1E+00	AW694933.1	EST HUMAN	QV06H0042-170300-165-g12 EN0042 Homo sapiens cDNA
1957	11763	21628	0.92	1.1E+00	AW576895.1	EST HUMAN	UHF-H00P-gk4f-02-01-51 NH JMG, 52 Homo sapiens cDNA clone IMAGE:3074834 3'
3289	13209	23009	6.61	1.1E+00	AL163219.2	NT	Homo sapiens chromosome 21 segment HS21C013
3288	13209	23010	6.61	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3441	13358	23185	0.93	1.1E+00	8622641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3510	13426	23185	1.26	1.1E+00	8622973	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3531	13447	23244	0.89	1.1E+00	AB06390.1	EST HUMAN	w64H1.41 Scores_NFL_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2559461 3' similar to
3957	13547	23357	1.19	1.1E+00	AE003896.1	EST HUMAN	SW-P031 HUMAN C12898 P93-BINDING PROTEIN SBP1 ;
3957	13571	23359	1.19	1.1E+00	AE003896.1	EST HUMAN	Xyella fastidiosa, section 32 of the complete genome
3978	13592	23378	17.81	1.1E+00	5729757	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3962	13773	23555	0.95	1.1E+00	8622641	NT	Homo sapiens calpain 9 (ncl-4) (CAPN9) mRNA
4122	14022	24520	5.80	1.1E+00	5935331	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4560	14740	24520	1.18	1.1E+00	U124185.1	NT	X.unicornis complete mitochondrial genome
4621	14800	24573	2.92	1.1E+00	U15466.1	NT	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds
							African swine fever virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4099	14874	24938	1.16	1.1E+00	X78425.1	NT	E. faecalis pfp5 gene
5249	19172	26045	1.57	1.1E+00	6978330	NT	Rattus norvegicus Aquaporin 4 (Aqp-4), mRNA
5448	19370	25426	12.04	1.1E+00	BE900194.1	EST HUMAN	00165277R1 NIH, MGC, 58 Homo sapiens cDNA clone IMAGE:3825835 3'
5460	19380	25440	1.29	1.1E+00	A1138952.1	EST HUMAN	q85c03.x1 Scores, basic, NHT Homo sapiens cDNA clone IMAGE:796260 3'
6422	19283	25444	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6422	19283	25445	1.93	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6435	19296	25459	7.63	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6729	19509	26799	3.22	1.1E+00	BF650996.1	EST HUMAN	002002562F1 NIH, MGC, 87 Homo sapiens cDNA clone IMAGE:4246628 5'
7659	17609	27733	1.65	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0924 protein, partial cds
7715	17565	27761	4.30	1.1E+00	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7744	17594	27815	20.08	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
8043	17834	28182	2.65	1.1E+00	11057364	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
8090	17981		3.41	1.1E+00	AF069942.1	NT	Xenopus laevis cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8447	13426		5.73	1.1E+00	8022973	NT	Homo sapiens hypothetical protein FL11280 (FL11280), mRNA
8450	18323	25581	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose 6-phosphate dehydrogenase 1 (G6PDH1), mRNA, complete cds
8450	18323	25582	4.41	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose 6-phosphate dehydrogenase 1 (G6PDH1), mRNA, complete cds
8562	18557	25635	4.73	1.1E+00	A030503.1	EST HUMAN	wf081.1.1 Scores, NFI, T, GGC, 51 Homo sapiens cDNA clone IMAGE:2861548 3'
9300	18959		4	1.1E+00	P07868	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
9402	19096	25310	2.13	1.1E+00	A1216996.1	NT	Tamias solutus immunoglobulin protein T516 mRNA, partial cds
9523	19570		1.54	1.1E+00	AF237169.1	NT	Dicystidium discolorum isopentenyl pyrophosphate isomerase (DipI), mRNA, complete cds
92	10077		3.49	1.0E+00	U29305.1	NT	Xenopus laevis histidine kinase, complete cds
105	10089	19004	1.14	1.0E+00	D98425.1	NT	Caixa colybae mRNA for serine/threonine kinase, complete cds
412	10358		2.19	1.0E+00	AE021694.1	NT	Mitochondrial polymerase gamma for 2S rRNA, 5S rRNA, 16S rRNA and 26S rRNA
562	10362	20308	1.14	1.0E+00	AJ251990.1	NT	Gardiera lignina mRNA for homeodomain transcription factor (so gene)
691	10585	20413	4.51	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
853	10597		0.95	1.0E+00	AF125964.1	NT	Aedes aegypti mucin-like protein MUC1, mRNA, complete cds
1384	12392		1.04	1.0E+00	X60416.1	NT	V. carteri Agg-2AM mRNA
1722	11523	21462	1.32	1.0E+00	AE006531.1	NT	Plasida still infestans virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2435	12312	22209	1.4	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2435	12312	22209	1.4	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2651	12518	22408	1.09	1.0E+00 AF131205.1	NT		Mus musculus Serf1 protein (Serf1), survival of motor neuron protein (Snm), neuronal apoptosis inhibitory protein-rs3 (NaiP-rs3), and neuronal apoptosis inhibitory protein-rs3 (NaiP-rs3) genes, complete cds
2846	12774	22591	3.48	1.0E+00 P24008	SWISSPROT		3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (3-STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2846	12774	22592	3.48	1.0E+00 P24008	SWISSPROT		3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (3-STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2938	12695		0.99	1.0E+00 O14229	SWISSPROT		HYPOPHETICAL 678 KD PROTEIN C8F128C IN CHROMOSOME I
3162	13067	22691	1.17	1.0E+00 A/A629483.1	EST_HUMAN		af25903.1 Soares, fetal, N23Hfs, Sw Homo sapiens cDNA clone IMAGE:1032830 3' similar to
3327	13247		0.81	1.0E+00 AF222781.1	NT		WP-C4208.3 CEM4204, contains element MER22 MER22 repetitive element;
3548	10077		1.15	1.0E+00 U123806.1	NT		Rattus norvegicus neuromedin U precursor (NimU) gene, exons 5 and 6
3627	13541	23328	1.44	1.0E+00 A/J23816.1	NT		Xenopus laevis rhodopsin gene, complete cds
3978	13895	23620	0.99	1.0E+00 AF223391.1	NT		Aegeria bisporus mRNA for lysozyme
4178	14078		0.79	1.0E+00 8022246	NT		Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4815	14698		0.88	1.0E+00 U/75741.1	NT		Homo sapiens hypothetical protein FLJ10135 (FLJ10135), mRNA
4931	14828		0.88	1.0E+00 U/75741.1	NT		Taeniopsis 48W antigen (TOW4) gene, complete cds
5139	15008	24777	0.97	1.0E+00 A/J235078.1	NT		Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5228	15162	24619	2.49	1.0E+00 Z07022.1	NT		Bacillus subtilis 42.7kb DNA fragment from ynfA to ynfA
5598	15484	25597	4.31	1.0E+00 AF248034.1	NT		Hordium vulgare gene encoding cysteine proteinase
5598	15484	25598	4.31	1.0E+00 AF248034.1	NT		Boa taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5719	15628	25728	4.82	1.0E+00 F04601	SWISSPROT		Boa taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5720	15627	25730	1.39	1.0E+00 A/1452782.1	EST_HUMAN		U-H-RS-arc-4-95-01 at NCI CGAP, Spid Homo sapiens cDNA clone IMAGE:306899 3'
5908	15914	25999	2.21	1.0E+00 U/75902.1	NT		Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 3, partial cds
6417	16279		8.49	1.0E+00 P20273	SWISSPROT		B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (SLYMPHOCTE CELL ADHESION MOLECULE) (BL-CAH)
6837	16306	26574	1.34	1.0E+00 AF192331.1	NT		Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
6846	16404	26583	5.09	1.0E+00 A/775101.1	EST_HUMAN		af76208.1 Stairagene lung (4837210) Homo sapiens cDNA clone IMAGE:868761 3'
6941	16521	26713	1.71	1.0E+00 BE698267.1	EST_HUMAN		001443950P1 INH. MGC_68 Homo sapiens cDNA clone IMAGE:3846005 5'
6941	16521	26714	1.71	1.0E+00 BE698267.1	EST_HUMAN		001443950P1 INH. MGC_68 Homo sapiens cDNA clone IMAGE:3846005 5'
6734	14628		1.38	1.0E+00 D10852.1	NT		Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds

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Probe SEQ ID NO.	Ecom SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source
6861	10740	29532	2.7	1.0E+00 Q02207		SWISSPROT
6861	16740	29833	2.7	1.0E+00 Q0207		SWISSPROT
6867	10496	27433	2.01	1.0E+00 BE147931.1	EST_HUMAN	PEROXISOMAL HYDROXYMETHYLGLUTARATE-DEHYDROGENASE-EPIMERASE (HDE) [MULTIFUNCTIONAL BETA-OXIDATION PROTEIN] (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D:3-HYDROXYACYL COA DEHYDROGENASE]
7064	16941	27133	1.9	1.0E+00 M38437.1	EST_HUMAN	Human immunodeficiency virus type 1 (HIV-1), isolate SF83.
7339	17397	27450	1.70	1.0E+00 BE507592.1	EST_HUMAN	B014975191 NF1 MAGC_70 Homo sapiens cDNA clone IMAGE:3856421 5'
7400	17320	27550	1.26	1.0E+00 G7634429	EST_HUMAN	Mut musclicus chloride channel calcium activated 1 (Clcat). mRNA
7480	17350	27527	1.26	1.0E+00 G7634429	EST_HUMAN	Mut musclicus chloride channel calcium activated 1 (Clcat). mRNA
7544	17395	27607	2.03	1.0E+00 AV680545.1	EST_HUMAN	AV680545 GKX Homo sapiens cDNA clone GIC001411 5'
7546	17397	27608	1.2	1.0E+00 U44832.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (ZPCP) mRNA, complete cds
7548	17397	27610	1.2	1.0E+00 U44832.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (ZPCP) mRNA, complete cds
7618	17766	28005	2.83	1.0E+00 AV758825.1	EST_HUMAN	BV758825 MAGC Homo sapiens cDNA clone BMFAW C04 5'
7695	17835	28075	17.08	1.0E+00 A2004982.1	EST_HUMAN	B044602.1 Scans_fetal liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
7696	17835	28076	17.08	1.0E+00 A2004982.1	EST_HUMAN	B044602.1 Scans_fetal liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
9130	18928		2.09	1.0E+00 P14300	SWISSPROT	THROMBOMODULIN PRECURSOR (TFMOUDOLIN) (TM)
9513	19126		1.51	1.0E+00 AV070184.1	EST_HUMAN	ESJ798293 MAGC resacques MAGC Homo sapiens cDNA
9689	19350		1.97	1.0E+00 A5006950.1	NT	Homo sapiens mRNA for KIAA1517 protein, partial cds
1503	11458	12135	0.84	9.9E-01 AF204455.1	NT	Drosophila melanogaster regulator of C-protein signalling LOC61111 mRNA, complete cds
1533	11458	12136	0.84	9.9E-01 AF204455.1	NT	Drosophila melanogaster regulator of C-protein signalling LOC61111 mRNA, complete cds
2568	12467	22360	0.9	9.0E-01 AF163022.2	NT	Homo sapiens chromosome 21 segment HS21C102
3453	13460		1.16	9.9E-01 AF174955.1	NT	Apple mosaic virus RNA-2 putative polymerase gene, complete cds
5461	13461	25441	9.22	9.9E-01 U64967	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
7336	17394		1.38	9.9E-01 U65097.1	NT	Lycopodium obscurum putative Mt copy 1 nematode-resistance gene
7510	17290		2.43	9.9E-01 Q28542	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
8067	17298	28237	2.02	9.9E-01 AJ006029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
1054	10454	20286	2.32	9.9E-01 P22967	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (NACE TYLGLOUTAMATE SYNTHASE) [AGCS] (NAGS)
512	10451	20286	2.32	9.9E-01 P22967	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (NACE TYLGLOUTAMATE SYNTHASE) [AGCS] (NAGS)
3732	13244	28429	0.82	9.9E-01 BE597439.2	EST_HUMAN	B01653683R2 NH_MAGC_55 Homo sapiens cDNA clone IMAGE:3833461 3'
3732	13244	28430	0.82	9.9E-01 BE597439.2	EST_HUMAN	B01653683R2 NH_MAGC_55 Homo sapiens cDNA clone IMAGE:3833461 3'
3732	13244	28430	0.82	9.9E-01 BE597439.2	EST_HUMAN	Enterobacteriaceae sp. JLM893 partial gcsS gene for GcsS-like protein and partial groEL gene for GroEL-like protein, isolate JM893
3272	16137	26292	4.91	9.9E-01 AJ302158.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2594	12494	22357	1.13	9.3E-01	BC071721	EST HUMAN	RC5-BT0503-271169-011-B01 BT0503 Homo sapiens cDNA
3949	13857	22830	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
3949	13857	22831	0.82	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
5155	15022		1.54	9.3E-01	AF075516.1	NT	Equus caballus microsatellite LE2013
5434	15354	25410	1.62	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5482	15402	25465	3.84	9.3E-01	L39189.1	NT	Spodoptera frugiperda methylglutathione S-transferase mRNA, complete cds
8701	16351	25771	1.85	9.3E-01	AA947040.1	EST HUMAN	cd05603.s1 NC1 CGAP O2 Homo sapiens cDNA clone IMAGE:1385357
9822	18325		1.55	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpL34 mRNA, complete cds
9854	18418		1.35	9.3E-01	BE32702.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAO/PH dehydrogenase-like protein (NSDHL), and L1>
3201	13125	22930	3.04	9.2E-01	BE32702.1	EST HUMAN	801441338T1 NIH MSC_72 Homo sapiens cDNA clone IMAGE:3516184.3
5943	15556	25849	4.23	9.2E-01	BF037566.1	EST HUMAN	801491158T1 NIH MSC_66 Homo sapiens cDNA clone IMAGE:3564461.5
7618	17469	27898	1.35	9.3E-01	6571677	NT	Mus musculus carbonic anhydrase 4 (Car4) mRNA
7990	17740	27933	3.63	9.2E-01	11430463	NT	Homo sapiens lysosomal sialylase-like protein 1 (LUSP1) mRNA
7952	17802	28041	1.73	9.2E-01	BF95251.1	EST HUMAN	7558406.s1 NC1 CGAP K341 Homo sapiens cDNA clone IMAGE:3575219.3 similar to SW:NU8M_TRYBB
8550	17677	25059	1.85	9.2E-01	BF132402.1	EST HUMAN	P04640 NUDH-LEUONINE OXIDOREDUCTASE CHAIN 5:
9068	18509	25701	2.01	9.2E-01	BF95047.1	EST HUMAN	801628312T1 NIH MSC_58 Homo sapiens cDNA clone IMAGE:4052018.5
2077	11957		1.43	9.1E-01	9523036	NT	80161575T1 NIH MSC_31 Homo sapiens cDNA clone IMAGE:429598.5
3160	13004	22959	0.97	9.1E-01	T29118.1	EST HUMAN	Homo sapiens hypophyseal protein FL20402 (PL20402), mRNA
3160	13004	22959	0.97	9.1E-01	T29118.1	EST HUMAN	AB2000GBR Infant brain, L1/L1L array of Dr. M. Soares (INB Homo sapiens cDNA clone LLA920028.5)
4310	13084	22899	0.97	9.1E-01	T25418.1	EST HUMAN	AB2000GBR Infant brain, L1/L1L array of Dr. M. Soares (INB Homo sapiens cDNA clone LLA920008.5)
4310	14207	23991	0.95	9.1E-01	U68172.1	NT	Rattus norvegicus mdr1 (MDR2) gene, partial cds
5919	15824	25950	2.92	9.1E-01	G61704	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
6472	15331	26498	15.99	9.1E-01	AA000023.1	EST HUMAN	cd71708.s1 NC1 CGAP G0B1 Homo sapiens cDNA clone IMAGE:1339592.3
6551	15409	26557	2.2	9.1E-01	AF02955.1	NT	Rattus norvegicus Rad3 GDP/GTP exchange protein mRNA, complete cds
9445	15924		30.05	9.1E-01	AF050113.1	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3170	13058	22900	0.89	9.0E-01	7691026	NT	Homo sapiens DKT27564M223 protein (DKT27564M223), mRNA
4282	14181	23959	2.37	9.0E-01	AF059810.1	NT	Homo sapiens neuron III-alpha gene, partial cds
4945	14822	24559	0.82	9.0E-01	AF017729.1	NT	Oryzopsis carolinensis Rad51 (RAD51) mRNA, complete cds
6385	15250		1.45	9.0E-01	D38621.1	NT	Xenopus laevis gene for adenosine, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5694	15413	25478	2.08	8.9E-01	AF020198.1	NT	Fugu ubriples neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
5766	15592		1.32	8.9E-01	X60068.1	NT	Rabbit MHC fragment RLA-DF DNA
5790	16794	20085	3.47	8.9E-01	AE003944.1	NT	Xyella fastidiosa, section 50 of 228 of the complete genome
5285	16937		4.74	8.9E-01	AE002166.2	NT	Chlamydomonas reinhardtii ARS9, section 21 of 84 of the complete genome
4442	14336	24126	3.29	8.9E-01	O28350	SWISSPROT	PURIFICATION-DEPENDENT NADP REDUCTASE
8430	16304	28550	2.98	8.9E-01	Z28337.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
9108	19722		1.76	8.9E-01	U00911.1	NT	Synedobrya sp. POC6903 complete genome, 1327, 1976503-171943
457	10401	20218	1.54	8.7E-01	AF100693.2	NT	Human sapiens SOST (SOST) gene, partial cds
2953	12233	22190	1.09	8.7E-01	5901889	NT	Human sapiens AT binding transcription factor 1 (ATBF1) mRNA
2945	12773	22560	4.84	8.7E-01	AA559983.1	EST_HUMAN	hmd5f1.1x1 NQ CGAP_P4-1 Homo sapiens cDNA clone IMAGE:076977
4935	14316		2.61	8.7E-01	AF121970.1	NT	Prokaryotic serine protease (serp), putative transcriptional regulatory protein Ohb8 (ohb8), ortho-helixerzelle 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-helixerzelle 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
7813	17484	27681	1.45	8.7E-01	AE010693.1	NT	Prokaryotic serine protease P401, section 524 of 559 of the complete genome
8205	18900	28343	5.47	8.7E-01	BE53070.1	EST_HUMAN	OV0.NR1021-100800-337-033 NN1021 Homo sapiens cDNA
8570	18716	25067	4.16	8.7E-01	BF107694.1	EST_HUMAN	80162568R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584.3
8570	18716	25068	4.16	8.7E-01	BF107694.1	EST_HUMAN	80162568R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043584.3
8488	19334		2.78	8.7E-01	AV051689.1	EST_HUMAN	AV051688 GLO Homo sapiens cDNA clone GLO01207.3
465	10409		1.08	8.6E-01	XT1702.1	NT	Rat 13F1 gene for insulin-like growth factor II
400	10787	20618	3.62	8.6E-01	W60069.1	EST_HUMAN	ad4403.11 Soares, fetal, heart, NHRH19W Homo sapiens cDNA clone IMAGE:343516.5
2224	12109	22012	1.01	8.6E-01	4903210	NT	Human sapiens cytochrome P450, subfamily XXVIII (steroid 27-hydroxylase, cerebrotendinous xanthomatase), polypeptide 1 (CYP27A1b) mRNA
3595	13482	23273	0.81	8.6E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3730	13842	23427	1.29	8.6E-01	UA6726.1	NT	Drosophila melanogaster medin (Dmedin) mRNA, complete cds
5595	15509	25889	11.82	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5955	15509	25887	11.82	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
5300	15934	20005	2.14	8.6E-01	AF143732.1	NT	Crus carolinensis recombinant activating protein 1 (RAG-1) gene, partial cds
6300	15934	20005	2.14	8.6E-01	AF143732.1	NT	Crus carolinensis recombinant activating protein 1 (RAG-1) gene, partial cds
6926	19300		1.02	8.6E-01	AF001518.1	NT	Bacillus halodurans genomic DNA, section 127/14
6443	16304	26469	2.79	8.5E-01	BE542812.1	EST_HUMAN	801071071 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:343505.5
7924	17774	28013	1.36	8.5E-01	AB000759.1	NT	Oryzopsis latifolia gene for SgC, complete cds
7924	17774	28014	1.36	8.5E-01	AB000759.1	NT	Oryzopsis latifolia gene for SgC, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9430	19643		2.02	8.4E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HNRP1), mRNA
9436	19076		2.03	8.5E-01	9607008	NT	Rattus norvegicus protein tyrosine phosphatases, non-receptor type 5 (Ptpn5), mRNA
9693	19238	26243	1.29	8.5E-01	AB030818.1	NT	Mus musculus mper1 gene for period1, complete cds
4108	14008	28795	0.84	8.4E-01	AF143506.1	NT	Mus musculus NK cell receptor 254, gene, promoter region and partial cds
5378	19443	25145	2.7	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
6378	19443	25146	2.7	8.4E-01	L78728.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7721	17571		3.13	8.4E-01	AJ245287.1	NT	P. troscoccus alysi complete genome, segment 5/6
724	10959	20489	2.37	8.3E-01	M83437.1	NT	Thermus thermophilus cytochrome c-452 (cycA) and CycB (cycB) genes, complete cds
3056	12383	22774	2.64	8.3E-01	AL161506.2	NT	Atadiplois italiana DNA chromosome 4, contig fragment No. 18
3739	13651	24434	1	8.3E-01	AB010870.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
3630	13339	23519	3.11	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
4917	14706	24570	1.12	8.3E-01	U46976.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB32
4917	14706	24571	1.12	8.3E-01	U46976.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB32
5177	14706	24570	0.95	8.3E-01	U46976.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB3
5177	14706	24571	0.95	8.3E-01	U46976.1	NT	Canis familiaris MHC DLA Class II DRB pseudogene DRB3
8222	16146	24339	2.13	8.3E-01	AL161540.2	NT	Xenopus laevis DNA chromosome 4, contig fragment No. 49
7573	17424		4.2	8.3E-01	AF79582.1	EST HUMAN	hncIT2.Y61 NC1, CQNP - Cof Homo sapiens cDNA clone IMAGE:1076466 5' similar to contains THR14 THR
7622	17672	27614	1.28	8.3E-01	AF068070.1	NT	Drosophila melanogaster L14 homolog mRNA, complete cds
7687	17717	27682	3.1	8.3E-01	AF108133.1	NT	Mus musculus neuro-24 gene, exons 3 through 12 and partial cds
8002	17938	28204	2.46	8.3E-01	AE000603.1	NT	Methanobacterium thermoautotrophicum from basiss 1270510 to 1283409 (section 109 of 148) of the complete genome
8070	17907		2.46	8.3E-01	7212472	NT	Physophthora infestans mitochondrion, complete genome
8623	19488	28760	2.03	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diesterinase triphosphate hydrolase (FHT) gene, exon 5
2008	11898	21769	2.69	8.2E-01	AB000469.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2943	12534		1.57	8.2E-01	AF145580.1	NT	Mus musculus trophoblast (Tm) gene, complete cds
2846	11953		1.14	8.2E-01	AF137690.1	EST HUMAN	IL3-C10219-167189-037-C08 C10219 Homo sapiens cDNA
5045	14917	24591		8.2E-01	AB000469.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
6122	10016	20154	3.29	8.2E-01	AF1379433.1	EST HUMAN	CMH-H10249-081199-037-001 HT0243 Homo sapiens cDNA
6309	19462	28330	3.59	8.2E-01	Z121238.1	NT	S. cerevisiae MET1, LEU4, and POL1 genes encoding MET1 (a protein, alpha-tropomyosin (alpha-TM) synthetase (partial), and DNA polymerase alpha (partial))
7768	17638	27871	1.53	8.2E-01	AF050593.1	NT	Homo sapiens fibronectin-related protein mRNA, complete cds
7637	17787	28028	6.63	8.2E-01	Q0170	SWISSPROT	MOX1/CK-KAUFMAN/BADEI-1/BED1 SYNDROMES PUTATIVE CHAPERONIN

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7837	17787	28029	6.65	8.2E-01	Q6U70	SWISSPROT	MOKUSIKKAUFMANBARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
8600	18717	29011	2.81	8.2E-01	L10127.1	SWISSPROT	Molluscan conglutinin virus type 1 ORF1 and ORF2 DNA
8965	18772	29084	6	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
8971	18777	29069	6.65	8.2E-01	H87386.1	EST HUMAN	yw-44022.1 Soares, placenta, Bsdwvskw, 2NkHrP8d0w Homo sapiens cDNA clone IMAGE:352185.5
9485	19383	28284	1.73	8.2E-01	AJ001261.1	NT	similar to gb:AF5072.0 G35 RIBOSOMAL PROTEIN L7A (HUMAN);
2731	12393	25284	1.29	8.1E-01	AF191838.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3412	13329	25130	2.81	8.1E-01	AF056936.1	NT	Homo sapiens MHC class 1 region
3412	13329	25131	2.81	8.1E-01	AF056936.1	NT	Homo sapiens MHC class 1 region
5992	15397	26020	2.49	8.1E-01	O13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN VG-B
5992	15397	26021	2.49	8.1E-01	O13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN VG-B
8773	15392	25879	1.84	8.1E-01	BE33658.1	EST HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
8773	15392	25880	1.84	8.1E-01	BE33658.1	EST HUMAN	RCO-TN0080-220800-025-410 TN0080 Homo sapiens cDNA
9168	19399	25343	1.84	8.1E-01	AJ271510.1	NT	Hemodigma malina section 23 of 136 of the complete genome
170	10142	20770	3.02	8.0E-01	AJ271510.1	NT	Shigella flexneri auresc partial pla gene for phosphatase kinase allele 15
285	10280	20070	3.78	8.0E-01	AJ271510.1	NT	Shigella flexneri auresc partial pla gene for phosphatase kinase allele 15
1990	11884	22761	1.83	8.0E-01	BF530621	EST HUMAN	902072473F1 NC1 COAP-Brn77 Homo sapiens cDNA clone IMAGE:4216941.5
3039	12397	22761	2.73	8.0E-01	BF530621	NT	902072473F1 NC1 COAP-Brn77 Homo sapiens cDNA clone IMAGE:4216941.5
3273	13194	22993	1.14	8.0E-01	AB005193.1	NT	Mus musculus gene for cdc42a glycoprotein, complete cds
3643	13357	24115	1.8	8.0E-01	AL162759.2	NT	Nasella meningidis serogroup A strain Z2497 complete genome, segment 777
4432	14327	24115	5.65	8.0E-01	X63759.2	NT	G. gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
6001	16341	20211	2.84	8.0E-01	AF160148.1	EST HUMAN	RCO-TN1015-270000-021-H06 NN1012 Homo sapiens cDNA
446	10380	20211	3.78	7.9E-01	D11476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
608	10351	20211	1.16	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 56 of the complete genome
687	11491	20211	65.97	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1634	11539	22009	1.37	7.9E-01	U32739.1	NT	Hemophilus influenzae Rd section 54 of 163 of the complete genome
2216	12102	22009	5.24	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitogenin29, complete cds
2217	12103	22007	2.29	7.9E-01	AF130459.1	NT	Danio rerio TPA-associated protein 1 ap1A (ap1A) mRNA, complete cds
3472	13388	23183	2.183	7.9E-01	AF229684.1	NT	Gallus gallus SOX9 transcription factor (SOX9) mRNA, complete cds
4204	14103	24103	0.92	7.9E-01	BE263672.1	EST HUMAN	601190333F1 NIH MSC-7 Homo sapiens cDNA clone IMAGE:3933786.5
4598	14401	24188	1.02	7.9E-01	BE263672.1	EST HUMAN	Mus musculus embp (Emb), mRNA
4598	14401	24188	1.02	7.9E-01	BE263672.1	EST HUMAN	Mus musculus embp (Emb), mRNA
5075	14045	24720	0.84	7.9E-01	Z47210.1	NT	S. pneumoniae fimb. capsA, capsB and capsC genes and cfs
5075	14045	24721	0.84	7.9E-01	Z47210.1	NT	S. pneumoniae fimb. capsA, capsB and capsC genes and cfs

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HR BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5084	14854		1.01	7.9E-01	M28500.1	NT	Human insulin receptor (dile 2) gene, exons 14, 15, 16 and 17
6721	15901	26790	2.43	7.9E-01	X09096.1	NT	P. salinus GR gene
7504	17373	27982	4.78	7.9E-01	U01912.1	NT	Cardiac lamella variant-specific surface protein C3M4-E (vspC3M4-E) mRNA, partial cds
7781	17631	27864	3.95	7.9E-01	P18719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
8372	18249		2.39	7.9E-01	769247.1	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
8543	18415	26892	2.48	7.9E-01	P18922	SWISSPROT	NEURAL-CADHERIN PRECURSOR (NCADHERIN)
859	10784		1.75	7.9E-01	Z43785.1	EST HUMAN	EST13KH01 normalized infant brain cDNA Homo sapiens cDNA clone c-18104
2229	12114	22019	3.2	7.9E-01	U195057.1	EST HUMAN	EST13KH01 MAGC sequences, MAGC Homo sapiens cDNA
4903	14487	24278	0.78	7.9E-01	AB17305.1	NT	Rattus norvegicus Transmembrane receptor UroSH1 mRNA, complete cds
5568	15807	25709	2.32	7.9E-01	AF118586.1	NT	Sphenodon punctatus alpha endonase mRNA, partial cds
7323	17189	27389	1.27	7.9E-01	Y10158.1	NT	D. discoideum recCAP gene
8424	18823		1.42	7.9E-01	L28280.1	NT	Arabidopsis thaliana 1-aminocyclopropane carboxylate synthase (ACS5) gene, complete cds
138	10112	18932	8.33	7.7E-01	AF184345.1	NT	Lyoparacanth hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
708	10841						Manurella major histocompatibility locus class II region major histocompatibility protein class II alpha chain (Alpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds
2050	12345	22435	1.85	7.7E-01	AF050187.1	NT	subunit alpha (NC2), hydrophilin-B
			2.8	7.7E-01	G53915	SWISSPROT	CITRATE SYNTHASE
3513	13234		0.8	7.7E-01	8894408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:poly(ADP-ribose) N-acetylglucosaminyltransferase 7 (GALNAc-T7) (GALNAc-T7), mRNA
3549	13484	23259	4.45	7.7E-01	AF115085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4297	14185	23679	2.98	7.7E-01	AF195488.1	NT	Colinus columba japonica sub-species japonica beta-actin mRNA, partial cds
4297	14186	23900	2.89	7.7E-01	AF195488.1	NT	Colinus columba japonica sub-species japonica beta-actin mRNA, partial cds
5415	15335	25390	1.44	7.7E-01	P10553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5415	15335	25397	1.44	7.7E-01	P10553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5626	15541	25630	1.95	7.7E-01	R09000.1	EST HUMAN	Y2402.1 Scores field liver spleen 1NLS Homo sapiens cDNA clone IMAGE:127755 3'
9212	10112	18932	2.6	7.7E-01	AF184345.1	NT	Lyoparacanth hirsutum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
9311	13004		6.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
5710	13018	25720	4.04	7.9E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCO3) mRNA, complete cds
5710	15518	25721	4.04	7.9E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCO3) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6669	19579	26770	1.41	7.9E-01	AF49793.2	NT	Mus musculus neuromedin U precursor (Nmn) gene, partial cds; TphLP (Tph) gene, partial cds; CLOCK (Clock) gene, complete cds; PFTZ7 (PFTZ7) gene, complete cds; and HBAR (HBar) gene, complete cds
6725	19006	26798	2.04	7.9E-01	6867752	NT	Mus musculus actinin (Actin-pending), mRNA
6726	19006	26797	2.04	7.9E-01	6867752	NT	Mus musculus actinin (Actin-pending), mRNA
7184	17061	27252	1.28	7.9E-01	6763371	NT	Mus musculus cytochrome P-450, 2d6, phenobarbital inducible, type 1 (Cyp2b9), mRNA
7347	17215	27414	7.62	7.9E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
7347	17215	27415	7.52	7.9E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
8684	18553	28837	2.31	7.9E-01	X96347.1	NT	M. aspersa mRNA for neurofilament NF70
8684	18553	28838	2.31	7.9E-01	X96347.1	NT	M. aspersa mRNA for neurofilament NF70
8948	18766	28838	4.81	7.9E-01	AL161592.2	NT	Xaibidopsis thaliana DNA chromosome 4, contig fragment No. 88
9073	18890		2.74	7.9E-01	AF020702.1	NT	Homo sapiens mRNA for KIAA0865 protein, partial cds
902	10444		1.52	7.9E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21G101
569	13508	20315	2.23	7.9E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHL1) gene, exon 5
3315	13238	22040	0.88	7.9E-01	G14293.1	EST HUMAN	Cl1293 Clontech human actin cDNA mRNA (85572) Homo sapiens cDNA clone GEN-037E11 5'
4573	10053	19500	13.92	7.9E-01	8928272	NT	Homo sapiens hypoxanthine phosphoribosyl transferase protein FL10793 (FL10793), mRNA
9351	19442		3.57	7.9E-01	AF163161.2	NT	Homo sapiens diaminodiphenylmethane precursor (DSPP) gene, complete cds
9528	19529	25209	1.87	7.9E-01	D9907.1	NT	Synchaetys sp. PC05053 complete genome, 3627, 1056497-118868
9584	19588	25190	1.42	7.9E-01	AE000932.1	NT	Methanocaldococcus thermophilus complete genome, 317350 to 328792 (section 29 of 148) of the complete genome
1114	11029	20669	1.23	7.9E-01	AI089446.1	EST HUMAN	h14093.1 NCI-GCAP Bm25 Homo sapiens cDNA clone IMAGE2161377 3' similar to contains Alu repetitive element/contains element MIR repetitive element;
2295	12177	22078	0.97	7.9E-01	AE01106.1	NT	Homo sapiens mRNA for KUD034 protein, partial cds
3695	13579	23368	1.22	7.9E-01	AF112538.1	NT	Human beta-actin (Act1) mRNA, complete cds
4213	14111	23889	4.43	7.9E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21G048
7295	17135	27328	7.23	7.9E-01	BE147503.1	EST HUMAN	0016700287 NIH_IMGC_9 Homo sapiens cDNA clone IMAGE3834174 5'
9041	18828		3.28	7.9E-01	AF763217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
9150	18901		1.50	7.9E-01	AUT72941.1	EST HUMAN	h1301.1 NCI-GCAP Bm25 Homo sapiens cDNA clone IMAGE2043985 3'
4515	14408	24194	0.95	7.9E-01	AE01106.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4002	14490	24277	4.76	7.9E-01	AF225421.1	NT	Homo sapiens HTO17 mRNA, complete cds
5127	14994		1.1	7.9E-01	5390211	NT	Homo sapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA
5684	15889	20010	5.61	7.9E-01	L33772.1	NT	Mus musculus antigen (CD72) gene
5684	15889	20011	5.61	7.9E-01	L33772.1	NT	Mus musculus antigen (CD72) gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6154	10315	26480	7.42	7.3E-01	M26511.1	NT	Valgynolous sucrose (erb) gene, complete cds
6454	10315	26481	7.42	7.3E-01	M26511.1	NT	Valgynolous sucrose (erb) gene, complete cds
8729	18395	26870	3.29	7.3E-01	AA678019.1	EST_HUMAN	22806a at Soares, fetal liver, spleen, 1NF15, S1 Homo sapiens cDNA clone IMAGE:431769 3'
8729	18395	26871	3.29	7.3E-01	AA678019.1	EST_HUMAN	22806a at Soares, fetal liver, spleen, 1NF15, S1 Homo sapiens cDNA clone IMAGE:431769 3'
814	10742		2.54	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (pif-2a) mRNA, complete cds
1914	11809	21687	3.68	7.2E-01	X79140.1	NT	A. tabacum Nif-4A13 mRNA
2412	12289	22186	1.46	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3029	12950	22746	1.19	7.2E-01	AF186100.1	NT	Fowlpox virus, complete genome
3406	13323	23124	2.14	7.2E-01	AF056506.1	NT	Gardia intestinalis variant-specific surface protein (vsp-417-6) gene, vsp-417-6(A-J) allele, complete cds
3795	13707	23494	1.31	7.2E-01	BF338330.1	EST_HUMAN	90203559P1 NCJ, CQAP, Bm54 Homo sapiens cDNA clone IMAGE:183222 5'
4660	14546	24335	2.41	7.2E-01	D60314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EO 2.4.1.7)
							Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptonemal complex cdc and L-type calcium channel α
5064	14934	24705	1.16	7.2E-01	AF196778.1	NT	Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T64 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptonemal complex cdc, and L-type calcium channel α
5064	14934	24707	1.16	7.2E-01	AF196778.1	NT	Cryptosporidium parvum P40S finger binding protein mRNA, partial cds
7623	15301	25994	1.21	7.2E-01	AF235051.1	NT	30271538FT NIH, MGC, 56 Homo sapiens cDNA clone IMAGE:4275881 5'
8121	18009	26295	4.78	7.2E-01	U82623.1	NT	Rattus norvegicus cyclophilin mRNA, complete cds
9570	19180		4.08	7.2E-01	AP0000683.1	NT	Aeropyrum pernix genomic DNA, section 877
							Rane calcitonin mRNA for bullfrog skeletal muscle calcium release channel (rymodine receptor) alpha isoform(RY1), complete cds
977	10010	20431	10.39	7.1E-01	D21070.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
3024	12952	22746	10.6	7.1E-01	AJ270777.1	NT	Mus musculus atropisin (Obog), mRNA
4114	14014	23793	2.93	7.1E-01	7905590	NT	Mus musculus atropisin (Obog), mRNA
4114	14014	23794	2.93	7.1E-01	7905590	NT	Mus musculus atropisin (Obog), mRNA
5623	15338	26626	1.56	7.1E-01	BF881034.1	EST_HUMAN	902715543FT NIH, MGC, 83 Homo sapiens cDNA clone IMAGE:4268344 5'
5623	15338	26626	1.56	7.1E-01	BF881034.1	EST_HUMAN	902715543FT NIH, MGC, 83 Homo sapiens cDNA clone IMAGE:4268344 5'
6149	15022	29162	6.97	7.1E-01	L83232.1	NT	Drosophila melanogaster 6-pyruvate/hydroxybutyrate synthase (pr) gene, complete cds
7099	17519	27746	2.25	7.1E-01	BE004005.1	EST_HUMAN	90146933FT NIH, MGC, 70 Homo sapiens cDNA clone IMAGE:3898465 5'
9363	19350		1.61	7.1E-01	AA427492.1	EST_HUMAN	3020711.51 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:731109 3'
1209	11118	20606	1.04	7.0E-01	AB014874.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1209	11118	20687	1.04	7.0E-01	AB014874.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2699	12277	22173	1.4	7.0E-01	N62412.1	EST_HUMAN	y73c07.s1 Soares, multiple, _adenoct_2NH-MSP Homo sapiens cDNA clone IMAGE:268708 3' similar to contains Alu repetitive element;
2699	12277	22174	1.4	7.0E-01	N62412.1	EST_HUMAN	y73c07.s1 Soares, multiple, _adenoct_2NH-MSP Homo sapiens cDNA clone IMAGE:268708 3' similar to contains Alu repetitive element
4089	14684		1.96	7.0E-01	AL163901.2	NT	Homo sapiens chromosome 21 segment HS21C101
8890	19799		8.1	7.0E-01	AE002283.1	NT	Escherichia coli K-12 MG1685 section 143 of 100 of the complete genome
8463	18336	26599	2	7.0E-01	AV1769842.1	EST_HUMAN	AV1769842 MDS Homo sapiens cDNA clone MDSCHB4 5'
8463	18336	26600	2	7.0E-01	AV1769842.1	EST_HUMAN	AV1769842 MDS Homo sapiens cDNA clone MDSCHB4 5'
954	10978	20725	15.73	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
954	10978	20726	15.73	6.9E-01	U69674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1289	11196	21049	2.21	6.9E-01	AA502630.1	EST_HUMAN	mi38309.s1 NCI CGAP_Gene1 Homo sapiens cDNA clone IMAGE:1085176 3'
3182	13107	22911	1.63	6.9E-01	AE002271.2	NT	Chemodan muridunum, section 3 of 86 of the complete genome
3399	13316	23117	0.85	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2511
8652	18332	20726	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8652	18332	20727	2.73	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8652	18490	26719	3.56	6.9E-01	D60103.1	NT	Homo sapiens DAN gene, complete cds
8652	18490	26720	3.56	6.9E-01	D60103.1	NT	Homo sapiens DAN gene, complete cds
9016	10543		2.37	6.9E-01	C09358	SWISSPROT	FOKHEAD BOX PROTEIN (C2) (FOKHEAD-RELATED PROTEIN FKHL4) (MESENCHYME FORK HEAD PROTEIN 1) (MFM-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL4)
941	10956	20713	1.03	6.9E-01	AF01724.1	NT	Gardia intestinalis caseinate lyase gene, complete cds
2699	12266		1.16	6.9E-01	U69671.1	NT	Synecocyst sp. PC2063 complete genome, 2127, 341855-3573470
2769	11502	21362	1.66	6.9E-01	AA064475.1	EST_HUMAN	y73c07.s1 Soares, parathyroid, tumor, N64FA Homo sapiens cDNA clone IMAGE:1402268 3' similar to p6-X69411, mat ALCOHOL DEHYDROGENASE QUASS (PI CHAIN [HUMAN]);
4469	14988	24163	1.26	6.9E-01	J007621.1	NT	Rat thymocyte protein gene: exon II and flanks
4749	14934	24420	0.83	6.9E-01	4759521	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
7556	17407	27622	1.52	6.9E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
8437	18311	26598	2.34	6.9E-01	AL127687.1	NT	Stagonopora aeneus bgl gene for beta-glucosidase, exon 1-4
8437	18311	26597	2.34	6.9E-01	AL127687.1	NT	Stagonopora aeneus bgl gene for beta-glucosidase, exon 1-4
8458	18331	26593	2.69	6.9E-01	AF136609.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8458	18331	26594	2.69	6.9E-01	AF136609.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8619	18465	26577	1.79	6.9E-01	AF164151.1	NT	Anopheles gambiae shem M2 translation initiation factor 4C (tIF-4C) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
295	10289	20060	28.34	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
339	10295	20110	19.03	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
2100	11989	21887	1.57	6.7E-01	AA471884.1	EST_HUMAN	Z120212.51 Soares_Kid_fetus_N02HF8_gw Homo sapiens cDNA clone IMAGE789310.3 similar to contains element TAR1 repetitive element;
2120	12713	21008	3.98	6.7E-01	AF18073.1	NT	Drosophila melanogaster Maf85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
2095	12693	22622	3.7	6.7E-01	667880	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4300	14246	24032	0.66	6.7E-01	X74431.1	NT	S. ubrocaum mRNA for glucose-6-phosphate dehydrogenase
4881	14762	24538	0.85	6.7E-01	AW079110.1	EST_HUMAN	vas5612.x1 NC1_OGAP_Cot17 Homo sapiens cDNA clone IMAGE257458.3
5182	15046	24811	0.89	6.7E-01	AL252942.1	NT	Dendrobium fimbriatum mRNA for phosphoenolpyruvate carboxylase, partial
5527	15542	25631	1.62	6.7E-01	AE001485.1	NT	Helicobacter pylori strain J99 section 47 of 132 of the complete genome
5817	15723	25836	1.42	6.7E-01	5835035	NT	Gallus herpesvirus 2, complete genome
5817	15723	25837	1.42	6.7E-01	5835035	NT	Gallus herpesvirus 2, complete genome
6329	16192	26337	3.98	6.7E-01	AE004505.1	NT	Pseudomonas aeruginosa PAO1, section 187 of 529 of the complete genome
6329	16192	26337	3.98	6.7E-01	AE004505.1	NT	Helicobacter pylori strain J99 section 47 of 132 of the complete genome
8323	18305	28149	2.23	6.7E-01	BF535489.1	EST_HUMAN	CX8-H10769-410605-197-c33 HT10/89 Homo sapiens cDNA
8754	17803	28147	3.69	6.7E-01	014357	SWISSPROT	N-ACEFYLGLUCOSAMINYL PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI
2452	12369	22237	0.87	6.8E-01	AF075249.1	NT	Homo sapiens SLT1 protein (SLT2) mRNA, partial cds
2587	12352	22422	1.29	6.8E-01	AF199381.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3445	13302	23108	1.04	6.8E-01	456680	NT	Homo sapiens lens domain, seven thymospondin repeats (Type 1 and Type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (benzophen) 9A (SEM5A) mRNA
3508	13522	23310	3.05	6.8E-01	Y07699.1	NT	C. albicans random DNA marker, 282bp
4020	13924		0.87	6.9E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rotor gene, and sodium phosphatase transporter (NP13) gene, complete cds
5825	15728	25840	3.96	6.8E-01	6680577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
6625	16384	26563	3.63	6.8E-01	AV060506.1	EST_HUMAN	AV060506 GLO Homo sapiens cDNA clone GLOCID4.3
7519	17422		2.41	6.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9671	19197	26296	1.35	6.8E-01	AE004382.1	NT	Vincio choline chromosome II, section 39 of 83 of the complete chromosome
608	10544	20352	1.37	6.8E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
608	10544	20353	1.37	6.8E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3386	13304	23104	5.1	6.9E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
3941	13869	22633	1.08	6.9E-01	4904632	NT	Human sapiens Interleukin 10 receptor, alpha (IL10RA) mRNA
4185	14085	23600	4.17	6.9E-01	AJ272285.1	NT	Homo sapiens SP-2 gene for secreted phosphoprotein 24 precursor, exons 1-3
4215	14113	23360	0.56	6.9E-01	AF161539.2	NT	Anaethesia Italiana DNA chromosome 4, contig fragment No. 39
4994	14669	24632	2.27	6.9E-01	U29821.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5175	15041		0.89	6.9E-01	U97258.1	NT	Acidobacter xylinum putative ATP binding protein delta-AccB gene, partial cds, and GDP-mannosylglyoxyl diphosphopyridoxal phosphate-dependent alpha-mannosyltransferase gene, complete cds
6036	15639	26071	1.38	6.9E-01	Q68348.1	NT	Chicken mRNA for 115-kDa melanocortin matrix protein, complete cds
7919	17708	28008	2	6.9E-01	AF116978.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
8030	17922	28198	3.24	6.9E-01	H97563.1	EST_HUMAN	HY17003.r1 Soares, placenta, 8dayweeks, 2N4HPEdW - Homo sapiens cDNA clone IMAGE:282816 5'
8073	17944	28216	4.03	6.9E-01	AJ601287.1	EST_HUMAN	nt1507.r1 NCL CGAP Phet Homo sapiens cDNA clone IMAGE:1100748 3'
8170	18658		4.27	6.9E-01	AI138078.1	EST_HUMAN	AU138078.PLACE1 Homo sapiens cDNA clone PLACE107810 5'
8877	19699	28631	2.3	6.9E-01	AF104115.1	NT	Phenothiazine biphosphate cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
8416	19069		2.79	6.9E-01	BE460350.1	EST_HUMAN	h14410.x1 NCL CGAP Luc3 Homo sapiens cDNA clone IMAGE:379133 3'
9581	18490		1.69	6.9E-01	U74146.1	NT	S cerevisiae chromosome IV coding frame ORF YOL0976
232	10218	20035	5.4	6.9E-01	U48946.1	NT	Drosophila melanogaster 5ld dyxen light chain mRNA, complete cds
3410	13527	23178	2.48	6.9E-01	U48946.2	NT	Mus musculus cytochrome C (CYC) gene, exons 1 and 2 and complete cds
3785	13607	23464	1.34	6.9E-01	AJ604627.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4399	14285	24066	0.84	6.9E-01	Y172488.1	NT	M. musculus win gene
4398	14285	24067	0.84	6.9E-01	Y172488.1	NT	M. musculus win gene
7007	16884	27078	1.78	6.9E-01	AC012427.1	NT	Tropomyosin pallidum section 03 of 87 of the complete genome
7807	17667	27695	13.62	6.9E-01	U82828.1	NT	Homo sapiens alpha telomerase (ATM) gene, complete cds
7818	17668	27696	1.44	6.9E-01	BF670405.1	EST_HUMAN	9021902891.NH.MGC_81 Homo sapiens cDNA clone IMAGE:4291128 5'
9528	19135		6.34	6.9E-01	AV769212.1	EST_HUMAN	9021902891.NH.MGC_81 Homo sapiens cDNA clone MDSGC09 5'
9951	19533		1.65	6.9E-01	9649300	NT	Rat cytochrome P-450, complete cds
427	10372	20196	4.41	6.9E-01	P05228	SWISSPROT	Rat cytochrome P-450, complete cds
624	10495	20277	2.15	6.9E-01	U52689.1	NT	Hemophilus influenzae Rd section 4 of 103 of the complete genome
2119	12005	21803	3.87	6.9E-01	U81136.1	NT	Shigella flexneri null-antibiotic resistance locus
2634	12408	22300	3.59	6.9E-01	U75331.1	NT	Galus galus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2834	12408	22301	3.59	6.9E-01	U75331.1	NT	Galus galus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2983	12911		0.93	6.9E-01	Y17276.1	NT	Lycopodium obscurum p6a gene, complete CDS

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3695	13892	23608	1.38	6.3E-01	X69676.1	NT	D melanogaster mRNA for melibiotropo glutamine receptor
6949	18937		3.17	6.3E-01	BE902044.1	EST HUMAN	g01079899f1 NH_MGC_21 Homo sapiens cDNA clone IMAGE:3060381 6'
7150	17027	27223	1.67	6.3E-01	S592927.1	NT	glycoprotein IIIa [JAL1 and 3 fusion junction] [Human, Genomic Mutant, 300 nt]
7421	17288	27495	2.72	6.3E-01	9627621	NT	Varicella virus, complete genome
7421	17288	27499	2.72	6.3E-01	9627621	NT	Varicella virus, complete genome
8004	17854	28005	1.4	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1655 section 203 of 400 of the complete genome
8413	18288	28543	2.27	6.3E-01	AA877116.1	EST HUMAN	m0908.01 NQ1_CGAP_Cor10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TRC02918 O02918
8647	18511	28791	11.72	6.3E-01	AI004160.1	EST HUMAN	HLARL :
8725	18591	28865	1.94	6.3E-01	P47003	SWISSPROT	CV4B7.0-3-360256-005 B1043 Homo sapiens cDNA
8869	18930	28969	1.68	6.3E-01	P39073	SWISSPROT	HYPOHETICAL13.3 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
9123	19697	24869	9.21	6.3E-01	P39073	SWISSPROT	HYPOHETICAL13.3 KD PROTEIN IN YMA12-APX1 INTERGENIC REGION
9220	18944		1.54	6.3E-01	AF108227.1	NT	Mus musculus testin complex 2, gene 9g (K12-9g), mRNA
9465	18919		1.68	6.3E-01	X63538.1	NT	Homo sapiens 3'-phosphoadenine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
9478	18403	25569	2.12	6.3E-01	Q10135	SWISSPROT	C. lividus pscD gene
9478	18403	25569	2.12	6.3E-01	Q10135	SWISSPROT	HYPOHETICAL142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
9531	19710	28903	3.05	6.2E-01	AF102233.1	NT	Mus musculus calcium-sensing receptor related protein-4 (CaSR-4) mRNA, partial cds
9531	19710	28903	3.05	6.2E-01	AF102233.1	NT	3x1003.51 Scores test liver spleen INFLS Homo sapiens cDNA clone IMAGE:215442 3'
7435	19448	28938	1.71	6.2E-01	BE595867.1	EST HUMAN	g01039160f1 NH_MGC_44 Homo sapiens cDNA clone IMAGE:596010 6'
7476	17336		2.66	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
7769	17546	27886	7.14	6.2E-01	AL161611.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
8007	17857	28099	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIO
8007	17857	28099	5.02	6.2E-01	P27410	SWISSPROT	PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2845	12226	28100	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIO
4831	14809	24577	0.96	6.1E-01	L20427.1	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Spac), mRNA
4831	14809	24577	0.96	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxydiphenylbenzoate methyltransferase mRNA, complete cds
6104	15998	28134	3.78	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6104	15998	28135	3.78	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6792	15971	20963	3.72	6.1E-01	AF033553.1	NT	Arabidopsis thaliana putative zinc transporter (ZPT) mRNA, complete cds
7108	16935	27176	1.76	6.1E-01	11431095	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
7108	16935	27176	1.76	6.1E-01	11431095	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
7419	17286	27492	19.47	6.1E-01	AF286117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
7419	17286	27493	19.47	6.1E-01	AF286117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7778	17928	27880	1.59	6.1E-01	AF18917.1	NT	Human dopamine transporter (SLC6A3) gene, complete cds
485	10429	20243	0.92	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
549	10490	20243	2.64	6.0E-01	S802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (GLA20) mRNA
1339	11245	21103	1.76	6.0E-01	AF056283.1	NT	Human respiratory syncytial virus strain CH63-45b attachment protein (G) gene, complete cds
3744	13955	23438	1.02	6.0E-01	AJ233968.1	NT	Viral hemagglutinin epitope virus N, P, M, G, Nv, L genes, French strain 07-71
5227	15151	24918	1.50	6.0E-01	P20238	SWISSPROT	D(2) DOPAMINE RECEPTOR
5339	15260	25089	2.58	6.0E-01	AW139713.1	EST_HUMAN	D(2) DOPAMINE RECEPTOR
5940	15845	25968	2.61	6.0E-01	U38913.1	NT	Musca domestica insecticide-susceptible stain voltage-sensitive sodium channel mRNA, complete cds
6350	16213	26375	6.2	6.0E-01	AJ270661.1	NT	Homo sapiens partial LMOT1 gene for LIM domain only/1 protein, exon 1
8725	18905	26704	4.19	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8723	18905	26705	4.19	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
7893	17503	27227	1.69	6.0E-01	AB009193.1	NT	Homo sapiens genes for leukotriens B4 receptor BLT2, leukotriens B4 receptor BLT1, complete cds
7894	17744	27227	1.43	6.0E-01	C01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PEROX (PEROXIN-3)
8411	18288	28541	1.78	6.0E-01	AJ311802.1	NT	Callus gallus mRNA for lysozyme protein, 416 ID isoform
8411	18288	28542	1.78	6.0E-01	AJ311802.1	NT	Callus gallus mRNA for lysozyme protein, 416 ID isoform
8538	19351	28542	2.74	6.0E-01	AH20023.1	EST_HUMAN	108107.X1 NCL COAP_P-229 Homo sapiens cDNA clone IMAGE289521.3'
9000	19115	25291	1.64	6.0E-01	11421693	NT	Homo sapiens nuclear factor (cytotoxic T-cell derived 2)-like 3 (NF2L3) mRNA
9787	19354	25085	2.1	6.0E-01	9053303	NT	Mus musculus cAMP-activated phosphodiesterase (Pde3), mRNA
6800	10484	20305	2.18	6.0E-01	BE157617.1	EST_HUMAN	108107.X1 NCL COAP_P-229 Homo sapiens cDNA clone IMAGE289521.3'
964	10907	20732	1.25	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3232	13156	22954	4.85	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
3232	13156	22955	4.85	5.9E-01	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C087
4129	14029		4.12	5.9E-01	AF162759.1	NT	Rattus norvegicus cecropin 2 mRNA, partial cds
5889	15795	25817	2.1	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
5891	17552	28203	2.67	5.9E-01	CGX003	SWISSPROT	THYMIDYLATE KINASE (TMP KINASE)
8328	18205	28454	3.1	5.9E-01	AW697175.1	EST_HUMAN	PM1-D10041-190100-302-03 DTD041 Homo sapiens cDNA
8529	18401	28569	2.39	5.9E-01	AF046265.1	NT	Mus musculus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
9105	19306	23342	1.91	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
9404	19307		2.19	5.9E-01	AB017705.1	NT	Aspergillus niger pyr G gene for criddle-5-phosphate dehydrogenase, complete cds
9914	19193		4.19	5.9E-01	P34928	SWISSPROT	Aspergillus niger pyr G gene for criddle-5-phosphate dehydrogenase, complete cds
1897	11783	21637	1.44	5.9E-01	P40472	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]

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3902	13812	26366	0.6	5.8E-01	BF686738.1	EST_HUMAN	601862477 INH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4413	14307	24090	2.81	5.8E-01	AF005077.1	NT	Vagina radialis mRNA for protein pyrophosphatase, complete cds
4690	14876		1.04	5.8E-01	AF110846.1	NT	Megastelia scabellata scabell homolog (Megs) gene, partial cds, alternatively spliced products
5763	15661	25768	1.26	5.8E-01	D78659.1	EST_HUMAN	HUM000508B Human placenta poly(A) (Tfujlwarh) Homo sapiens cDNA clone GEN500509 5'
6077	16000		2.3	5.8E-01	BF50961.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1330 nt]
6904	16164		2.62	5.8E-01	H41871.1	EST_HUMAN	yH1103 s1 Scores adult brain N26SH3557 Homo sapiens cDNA clone IMAGE:175767 5' similar to
6764	16543	26630	2.23	5.8E-01	F14328	SWISSPROT	gb:578187 M-PHASE INDUCER PHOSPHATASE 2 (-HUMAN);
6764	16543	26630	2.23	5.8E-01	F14328	SWISSPROT	SPORE COAT PROTEIN SP95
7163	17030	27224	8.64	5.8E-01	AJ270774.1	NT	Homo sapiens partial TOF-4 gene for 1-cell transcription factor-4, exon 8-11
8398	18265	28463	8.47	5.8E-01	AJ243213.1	NT	Homo sapiens partial G-HF-4 receptor gene, exon 2 to 6
8398	18272	28463	3.23	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 INH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
8482	18365		1.78	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 INH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
3195	13111	22616	1.46	5.7E-01	Q9WTL2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVOL-KE-1 (MOV01) (MOV01A)
3450	13376		2.43	5.7E-01	AF935503.1	NT	Populus alamosiana pease-2 mRNA for 1-aminopyridoxase-1-carboxyle synthase, complete cds
3629	13741	23633	1.06	5.7E-01	AF011581.1	NT	Homo sapiens 1 cell receptor beta chain (B06872) (B151) mRNA, partial cds
5201	15064	24827	2.24	5.7E-01	U76187.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEF1) mRNA, partial cds
5838	15742	23954	3.72	5.7E-01	BF039413.1	EST_HUMAN	601456025F1 INH_MGC_56 Homo sapiens cDNA clone IMAGE:385550 5'
6100	15110	24874	1.41	5.7E-01	AL111440.1	NT	Bostrychia ciliata strain T4 cDNA library under conditions of nitrogen deprivation
6664	16422	26603	2.12	5.7E-01	P00373	SWISSPROT	PROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5CR REDUCTASE)
9124	18863		1.68	5.7E-01	BE716091.1	EST_HUMAN	MF43-H10735-18700-003-402 H10735 Homo sapiens cDNA
3318	13239	23043	1.21	5.6E-01	AF016293.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3318	13239	23044	1.21	5.6E-01	AF016293.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3608	13720	23509	0.83	5.6E-01	AF161601.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
4148	14045	23818	0.83	5.6E-01	D63135.1	NT	Chicken TBP gene, exon6, complete cds
7111	18688	27180	4.16	5.6E-01	AF064703.1	EST_HUMAN	AV084703.3 GKX Homo sapiens cDNA clone GKXFS08 5'
7111	18688	27181	4.16	5.6E-01	AF064703.1	EST_HUMAN	AV084703.3 GKX Homo sapiens cDNA clone GKXFS08 5'
5023	18817		2.46	5.6E-01	BE886280.1	EST_HUMAN	601544007F1 INH_MGC_71 Homo sapiens cDNA clone IMAGE:3916457 5'
9137	18663	28704	1.73	5.6E-01	AA465935.1	EST_HUMAN	ntf5g10.s1 NC1 CGAG_P16 Homo sapiens cDNA clone IMAGE:940674 similar to contains element PTR7 repetitive element ;
5624	19133		1.32	5.6E-01	F59005	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
5919	19392		3.09	5.6E-01	BF56382.1	EST_HUMAN	602132622F1 INH_MGC_81 Homo sapiens cDNA clone IMAGE:4271834 5'

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1193	11103	20949	1.09	5.9E-01	8393912	NT	Radius nonregious Propriety Coenzyme A carboxylase beta polypeptide (PcoB), mRNA
2698	12533	22423	2.88	5.9E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2698	12533	22424	2.88	5.9E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2988	12815	22208	1.34	5.9E-01	5902085	NT	Homo sapiens superfamily viral-like activity 2 (S. cerevisiae homolog), like (SKIV2L), mRNA
3027	12565	22526	1.39	5.9E-01	H46219.1	EST_HUMAN	yo1810.61 Scores adult brain N2051B557 Homo sapiens cDNA clone IMAGE:178268 3'
3196	13121	22526	3.1	5.9E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3934	13548	23335	1.29	5.9E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
139	10113	10333	3.74	5.4E-01	7957268	NT	Homo sapiens KIAA0029 protein Mac2 interacting nuclear target (MINT) homolog (KIAA0029), mRNA
139	10113	19634	3.74	5.4E-01	7957268	NT	Homo sapiens KIAA0029 protein Mac2 interacting nuclear target (MINT) homolog (KIAA0029), mRNA
570	10508	20318	2.61	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
570	10508	20317	2.61	5.4E-01	AF232008.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
1269	11157	21006	2.24	5.4E-01	AF165097.1	EST_HUMAN	DNA/RNA/DNA/070300-180-234 NN0040 Homo sapiens cDNA
2058	13498	21908	2.78	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae A1936, section 74 of the complete genome
2303	12093	21908	2.23	5.4E-01	AJ276662.1	NT	Proxymyces medusae sp. mRNA for 18.15' beta, contains dihydroxy acid (beta-diox) gene
7738	17388	26557	2.01	5.4E-01	BF972535.1	EST_HUMAN	062075658F1 NH, MGC 32 Homo sapiens cDNA clone IMAGE:423980 5'
8427	16301	26557	2.87	5.4E-01	P36863	SWISSPROT	NITRATE REDUCTASE (NADPH) (NR)
8592	16702	26666	4.51	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
8592	16702	26597	4.51	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
9087	18992		2.12	5.4E-01	A1858308.1	EST_HUMAN	M87604.1 NQ, CGAP_UH Homo sapiens cDNA clone IMAGE 2427126 3' similar to gp134/2 LAMIN A (HUMAN);
905	10447	20260	2.02	5.9E-01	AF109413.1	NT	Homo sapiens HLA class II region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) 311, helicase (SKIV2), RD, complement factor B (Bf), and complement component C2 (C2) genes;>
2093	11882	21877	0.91	5.9E-01	AF113919.1	NT	Bresla deiracosa var. capitata phospholipase D2 (PLD2) gene, complete cds
2093	11882	21878	0.91	5.9E-01	AF113919.1	NT	Bresla deiracosa var. capitata phospholipase D2 (PLD2) gene, complete cds
2755	12517	22508	8.24	5.9E-01	4500328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zein polypeptide 1 (PTPRZ1) mRNA
2755	12517	22509	8.24	5.9E-01	4500328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zein polypeptide 1 (PTPRZ1) mRNA
3205	13129	22531	2.92	5.9E-01	AF107658.1	NT	Homo sapiens secreted C-type lectin precursor (SLCCL) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4117	14017		1.29	6.3E-01	U36987.1	NT	Myoplasma genitalium section 9 of 61 of the complete genome
5360	15270	20088	1.75	5.3E-01	AI020921.1	EST_HUMAN	2u2H12.6 Scores over tumor NHHOT Homo sapiens cDNA clone IMAGE:740711 5'
5360	15270	20069	1.75	6.3E-01	AI020921.1	EST_HUMAN	2u2H12.6 Scores over tumor NHHOT Homo sapiens cDNA clone IMAGE:740711 5'
5467	16387	25447	1.91	5.3E-01	BE646520.1	EST_HUMAN	7a73c12x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:3285118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5467	16387	25448	1.91	5.3E-01	BE646520.1	EST_HUMAN	7a73c12x1 NCI CGAP P128 Homo sapiens cDNA clone IMAGE:3285118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
7161	17038		2.15	5.3E-01	L01050.2	NT	Sordaria apocryptes ribulose 1,5-bisphosphate carboxylase (rbcL) gene, partial cds, chloroplast gene for chloroplast product
8946	18958	28946	5.62	5.3E-01	BE569201.1	EST_HUMAN	80133687F1 NH MGCC 53 Homo sapiens cDNA clone IMAGE:3582168 5'
9015	19551		2.45	5.3E-01	AA091953.1	EST_HUMAN	80133687F1 NH MGCC 53 Homo sapiens cDNA clone IMAGE:3582168 5'
793	10728	20668	11.31	5.2E-01	L20770.1	NT	APOLIPROTEIN D PRECURSOR (HUMAN);
1148	11081	20804	7.69	5.2E-01	Q0M120	SWISSPROT	Drosophila melanogaster hank-100-hk1 mRNA, complete cds
1174	11085	20750	2.83	6.2E-01	AF224062.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 3 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-A15) PREL-DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5
1543	11739		5.04	5.2E-01	AL103263.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2069	11868	21865	2.78	5.2E-01	AB012853.2	NT	Homo sapiens mRNA for KMA0740 protein, partial cds
3087	13008	22708	1.93	5.2E-01	U65942.1	NT	Chlamydomonas reinhardtii strain S205 POMP-5A and POMP-5A precursor, genes, complete cds
3100	13124		1.22	5.2E-01	D73443.1	NT	Azobacter vinelandii lat gene for isochlorogenic acid, complete cds
3369	13278		1.76	5.2E-01	AL116780.1	NT	Borhya cheria strain T4 cDNA library under conditions of nitrogen deprivation
3397	13314	23114	1.9	5.2E-01	AA694165.1	EST_HUMAN	am7905.11 Stratiocetes schizos brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
3680	13494		1.13	5.2E-01	AF020269.1	NT	Medicago sativa chloroplast male dehydrogenase precursor (p1mch) mRNA, nuclear gene encoding chloroplast protein, complete cds
3682	13498	23287	1.05	5.2E-01	U62071.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L12
4840	14926		1.29	5.2E-01	7108444	NT	Mus musculus ventral receptor-like protein 1 (VRL1), mRNA
7719	17811	27837	1.28	5.2E-01	AF143965.2	EST_HUMAN	Homo sapiens PELOTA (PELOTA) gene, complete cds
9719	19200	20221	2.46	5.2E-01	AF137093.1	NT	U-H-B1 sup-e-08-0-UJ-31 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2714769 3'
9837	19370		3.43	5.2E-01	P18516	SWISSPROT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
901	10537	20347	1.89	5.1E-01	M68609.1	NT	Human adrenomedullin reductase gene, exons 3 to 12
632	10599	20381	3.28	5.1E-01	A123894.1	NT	Polyomavirus stitulum (strain PI 40) 16S rRNA gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
772	10702	20541	1.98	4.9E-01	BF571462.1	EST_HUMAN	606207684Ft NIH_LMGC_60 Homo sapiens cDNA clone IMAGE:4243860 5'
1864	11760	21634	1.36	4.9E-01	U400693.1	NT	Centri podocilia pulmonary surfactant protein A (SP-A) mRNA, complete cds
5979	19598	25998	2.46	4.9E-01	AF020693.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5979	19598	25999	2.46	4.9E-01	AF020693.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6408	16207	26420	1.76	4.9E-01	AB040067.1	NT	Oryza sativa subsp. japonica mif-G mRNA for mitochondrial elongation factor G, complete cds
7107	17074		1.41	4.9E-01	BF260791.1	EST_HUMAN	801874684Ft NIH_LMGC_54 Homo sapiens cDNA clone IMAGE:4102603 5'
7369	19709		2.2	4.9E-01	U048863	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13n1), mRNA
6065	18346		1.43	4.9E-01	AF170912.1	NT	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
9951	19733		3.56	4.9E-01	AA613562.1	EST_HUMAN	hg22et11.51 NGL CGAP_C010 Homo sapiens cDNA clone IMAGE:114652 3'
							Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated product
4577	14136		1.12	4.9E-01	4904830	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
5381	15300	20163	8.94	4.9E-01	J02967.1	NT	ms5f69a.ct NGL CGAP_AV1 Homo sapiens cDNA clone IMAGE:1217613
6719	15922		3.94	4.9E-01	AA65878.1	EST_HUMAN	Homo sapiens reproduction 5 (DRS2293E) mRNA
8030	19193		1.96	4.9E-01	5031650	NT	Xenopus laevis DNA chromosome 4 contig fragment No. 4
8563	16421	26801	3.82	4.9E-01	AL161492.2	NT	Xenopus laevis DNA chromosome 4 contig fragment No. 4
8565	16421	26802	3.82	4.9E-01	AL161492.2	NT	Xenopus laevis DNA chromosome 4 contig fragment No. 4
6613	18468	26879	1.16	4.9E-01	AI820744.1	EST_HUMAN	17710.yf Scores breast ZNF484 Homo sapiens cDNA clone IMAGE:164795 5' similar to contains element
8111	18301		2.04	4.9E-01	X65002.1	NT	S. cerevisiae ORF's from chromosome X
9369	19311		2.52	4.9E-01	AF227636.1	NT	Hypocretin class transposon VIP II SIRE repeat region
9570	19359		2.28	4.9E-01	BE790632.1	EST_HUMAN	80184524Ft NIH_LMGC_7 Homo sapiens cDNA clone IMAGE:3935909 5'
6525	19399	25053	8.39	4.7E-01	BF217183.1	EST_HUMAN	80186886Ft NIH_LMGC_57 Homo sapiens cDNA clone IMAGE:4063887 5'
8221	18103		5.77	4.7E-01	AF102873.1	NT	Influenza A virus isolate h671697 hemagglutinin (HA) gene, partial cds
8434	18308	28564	2.03	4.7E-01	U41009.1	NT	Human collagen alpha2(V) (COL1A2) gene, exons 6 through 16, and partial cds
8692	18570	29363	2.46	4.7E-01	AW899448.1	EST_HUMAN	RCBNT0029-240400-01-E08 NT0029 Homo sapiens cDNA
9390	19348		1.36	4.7E-01	AW341581.1	EST_HUMAN	RC11608.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2806188 3'
3674	19398	23376	1.27	4.6E-01	AW818038.1	EST_HUMAN	RC1-S10275-040400-016-006 ST0278 Homo sapiens cDNA
3683	19397	23383	1.26	4.6E-01	AF663300.1	EST_HUMAN	802081108Ft NIH_LMGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3683	19397	23384	1.26	4.6E-01	AF663300.1	EST_HUMAN	802081108Ft NIH_LMGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5087	14957		0.97	4.6E-01	MT11267.1	NT	Bovine steroid 12-hydroxylase gene (p-450-c21) gene, complete cds
5360	15230	25111	3.39	4.6E-01	Q00643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5360	15230	25112	3.39	4.6E-01	Q00643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5147	15323	26372	1.78	4.6E-01	BE734761.1	EST_HUMAN	801569735Ft NIH_LMGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5414	16334	25394	3.29	4.9E-01	A127079.1	EST_HUMAN	q10h02.x1 Soares, fetal liver, spleen, ³ INFLS, ³ 1 Homo sapiens cDNA clone IMAGE:1849011 ³ similar to TR-O15338 O15338 BUTYRPHILIN ;
5414	16334	25395	3.29	4.9E-01	A127079.1	EST_HUMAN	q10h02.x1 Soares, fetal liver, spleen, ³ INFLS, ³ 1 Homo sapiens cDNA clone IMAGE:1849011 ³ similar to TR-O15338 O15338 BUTYRPHILIN ;
5418	16339	25393	1.56	4.9E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1 ;
6057	16040	20161	1.47	4.9E-01	U02332.1	NT	Emertella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6057	16040	20182	1.47	4.9E-01	U02332.1	NT	Emertella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6943	16722	20010	13.48	4.9E-01	BF597369.1	EST_HUMAN	902130583F NIH MGSC 56 Homo sapiens cDNA clone IMAGE:4287828 ⁵
7393	17230	27430	26.48	4.9E-01	P95202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7393	17230	27431	26.48	4.9E-01	P95202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7730	17590	27802	1.33	4.9E-01	A1016934.1	EST_HUMAN	w073a12.x1 Soares, NSF, F8, 9W, OT, PA, P, ³ 1 Homo sapiens cDNA clone IMAGE:2370768 ³
7730	17590	27803	1.33	4.9E-01	A1016934.1	EST_HUMAN	w073a12.x1 Soares, NSF, F8, 9W, OT, PA, P, ³ 1 Homo sapiens cDNA clone IMAGE:2370768 ³
8359	18238	25495	2.86	4.9E-01	P08163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
8369	18246	25495	4.78	4.9E-01	BE185446.1	EST_HUMAN	UL5-H70730-105504-975-g08 H70730 Homo sapiens cDNA
8369	18246	25495	4.78	4.9E-01	BE185446.1	EST_HUMAN	UL5-H70730-105504-975-g08 H70730 Homo sapiens cDNA
8703	17015	22160	5.45	4.9E-01	AF010359.1	NT	Human thymidine methyltransferase (TMT) gene, exon 10 and complete cds
8703	17015	22161	5.45	4.9E-01	AF010359.1	NT	Human thymidine methyltransferase (TMT) gene, exon 10 and complete cds
8813	10006		1.43	4.9E-01	D63316.1	EST_HUMAN	HUM1067035 Clontech human fetal brain polyA+ mRNA (46305) Homo sapiens cDNA clone GEN-105F03 ⁵
9078	19491		2.21	4.9E-01	AF120134.1	NT	Unifluor jamaicensis melutase (melF) gene, chloroplast gene encoding chloroplast protein, partial cds
1869	11765	21639	1.73	4.9E-01	AEO01631.1	NT	Drosophila melanogaster R1 section 68 of 229 of the complete chromosome 1
1869	11765	21640	1.73	4.9E-01	AEO01631.1	NT	Drosophila melanogaster R1 section 68 of 229 of the complete chromosome 1
2841	12769	22598	4.87	4.9E-01	AA67096.1	EST_HUMAN	q554002.x1 Soares, fetal liver, spleen, ³ INFLS, ³ 1 Homo sapiens cDNA clone IMAGE:454719 ³
3375	13198	22068	3.97	4.9E-01	Q06703	SWISSPROT	PRECURSOR (HSPG) (PERLECAN) (PLC)
3331	13251	23056	1.05	4.9E-01	AF120378.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
3942	13950		1.41	4.9E-01	Q28247	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN
3982	13989	22655	1.1	4.9E-01	AF108906.1	EST_HUMAN	5560609.x1 Barlsted scRNA HPIR618 Homo sapiens cDNA clone IMAGE:2363480 ³
4086	15079		4.02	4.9E-01	AW873495.1	EST_HUMAN	h030202.x1 Soares, NFL, T, GBC, ³ 1 Homo sapiens cDNA clone IMAGE:3041810 ³

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mod Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4862	14742	24522	0.94	4.9E-01	BE95445.2	EST_HUMAN	80165729R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3968023 3'
5106	15325	29376	1.47	4.9E-01	AF028814.1	EST_HUMAN	710217012-140100-031-039 PT0012 Homo sapiens cDNA
5693	15839		1.45	4.9E-01	Q100565	SWISSPROT	COAT PROTEIN
6488	16346	26515	2.49	4.9E-01	A1859845.1	EST_HUMAN	M32402.1 NCL CGAP_U1 Homo sapiens cDNA clone IMAGE:2429618 3' similar to TR:Q29233 Q29233
6967	16776	26970	3.14	4.9E-01	A1448596.1	EST_HUMAN	SWISNSF COMPLEX 170 KDa SUBUNIT ;
7100	16977		1.54	4.9E-01	11444780	EST_HUMAN	U5911.1 NCL CGAP_OX35 Homo sapiens cDNA clone IMAGE:2292644 3'
7891	17841	26282	25.09	4.9E-01	M86055.1	EST_HUMAN	Homo sapiens hypothetical protein D16725.47/183 DKFZ547G183, mRNA
7891	17841	26003	25.09	4.9E-01	M86055.1	EST_HUMAN	EST102631 Fetal brain, Striatum (cDNA393205) Homo sapiens cDNA clone HFB0Y17
8327	18117	26869	2.42	4.9E-01	AW591271.1	EST_HUMAN	EST102631 Fetal brain, Striatum (cDNA393205) Homo sapiens cDNA clone HFB0Y17
9036	19724		2.25	4.9E-01	BE871451.1	EST_HUMAN	901491.1 NCL CGAP_U18 Homo sapiens cDNA clone IMAGE:2709965 3' similar to SW:JNT6_MOUSE
9694	19245		1.44	4.9E-01	BF337531.1	EST_HUMAN	064222 VIRAL INTEGRATION SITE PROTEIN NT-6 [1];
9763	19283		2.15	4.9E-01	11422388	EST_HUMAN	064222 VIRAL INTEGRATION SITE PROTEIN NT-6 [1];
9674	19952	24987	1.83	4.9E-01	AF23224.2	EST_HUMAN	80144202 F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3482281 5'
1091	11685		2.47	4.9E-01	6690303	NT	80230276 F1 NCL CGAP_Bmp24 Homo sapiens cDNA clone IMAGE:4183220 5'
2540	12220	22118	3.99	4.4E-01	P49705	SWISSPROT	Homo sapiens beta-specific lipase 2 (TESK2), mRNA
3274	13195	22954	0.99	4.4E-01	AF058790.1	NT	Human histophilic alveolar protein (HAP) gene, partial cds
3274	13195	22955	0.99	4.4E-01	AF058790.1	NT	Mac mucusin integral membrane-associated protein 1 (Imagp1), mRNA
3277	13198	22958	1.87	4.4E-01	BF066726.1	EST_HUMAN	VASCULAR ENDOTHELIAL GROWTH FACTOR 8 PRECURSOR (VEGF-8) (VEGF RELATED FACTOR)
4141	14041		1.33	4.4E-01	BE378727.1	EST_HUMAN	Rattus norvegicus SynGAP-5 mRNA, complete cds
4924	14813		0.93	4.4E-01	BE141396.1	EST_HUMAN	Rattus norvegicus SynGAP-5 mRNA, complete cds
5326	15246	25050	1.99	4.4E-01	P04629	SWISSPROT	7916122 F1 NIH_MGC_24 Homo sapiens cDNA clone IMAGE:3303766 5'
5326	15246	25051	1.89	4.4E-01	P04629	SWISSPROT	80123719R1 NCL CGAP_Bmp24 Homo sapiens cDNA clone IMAGE:3603693 5'
5460	15409	25474	1.3	4.4E-01	S605120	NT	MRQ-H0078-131289-007-405 HT0078 Homo sapiens cDNA
5469	15418	25481	1.93	4.4E-01	AV120408.1	EST_HUMAN	MRQ-H0078-131289-007-405 HT0078 Homo sapiens cDNA
5924	15539	25927	1.6	4.4E-01	A1186413.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5924	15539	25928	1.6	4.4E-01	A1186413.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5782	15659	26706	1.79	4.4E-01	AV080705.1	EST_HUMAN	Human [Rats, Sprague-Dawley, sulfur dioxide-treated tracheal epithelium, mRNA, partial, 300 nt]
5832	16462		10.84	4.4E-01	Z11679.1	NT	AV120408 GLC Homo sapiens cDNA clone GLCOS12 5'
							902011.1 NCL CGAP_Bmp25 Homo sapiens cDNA clone IMAGE:1961125 3' similar to TR:Q29168 Q29168
							UNKNOWN PROTEIN ;
							902011.1 NCL CGAP_Bmp25 Homo sapiens cDNA clone IMAGE:1961125 3' similar to TR:Q29168 Q29168
							UNKNOWN PROTEIN ;
							902011.1 NCL CGAP_Bmp25 Homo sapiens cDNA clone IMAGE:1961125 3' similar to TR:Q29168 Q29168
							UNKNOWN PROTEIN ;
							902011.1 NCL CGAP_Bmp25 Homo sapiens cDNA clone IMAGE:1961125 3' similar to TR:Q29168 Q29168
							UNKNOWN PROTEIN ;
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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7354	17222	27422	1.28	4.4E-01	Q62836	SWISSPROT	ZINC FINGER XCHROMOSOMAL PROTEIN
7723	17673	27766	1.98	4.4E-01	A1368950.1	EST HUMAN	q68060.1 NCI CGAP L16 Homo sapiens cDNA clone IMAGE:1810821 3'
7724	17674	27767	2.45	4.4E-01	E29822	SWISSPROT	GLYOPROTEIN B PRECURSOR (GLYOPROTEIN 14)
7813	17693	27603	4.97	4.4E-01	P33560	SWISSPROT	"YROSINE-PROTEIN KINASE RECEPTOR TIE-1" PRECURSOR
7935	17785	28025	1.33	4.4E-01	U79404.1	NT	beta-HKA-H1(KA)Pase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
7935	17785	28026	1.33	4.4E-01	U79404.1	NT	beta-HKA-H1(KA)Pase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
9260	18098	28528	2.28	4.4E-01	6677814	NT	MA muscularium sodium channel, type X, alpha polypeptide (Sm10a), mRNA
9308	18083	28528	3.28	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21, segment H821C082
9731	12687	26224	5.34	4.4E-01	6827742	NT	Autographa californica nucleopolyhedrovirus, complete genome
9731	12628	26224	1.76	4.4E-01	P64726	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD28 HOMOLOG A (HR23A)
405	10351	20178	1.98	4.3E-01	AF152181.1	NT	Callitrix jacchus MWALW opsin genes, upstream flanking region
405	10351	20179	1.98	4.3E-01	AF152181.1	NT	Callitrix jacchus MWALW opsin genes, upstream flanking region
1586	11498	21590	1.11	4.3E-01	AW 66566.1	EST HUMAN	Q745N0024:200400-163-201 SN0024 Homo sapiens cDNA
2843	12771	26025	0.68	4.3E-01	AW 665208.1	EST HUMAN	CM2-170008-010300-077-031 DT0003 Homo sapiens cDNA
3022	12860	22742	0.93	4.3E-01	AW 699477.1	EST HUMAN	MF0-SN0070-276000-008-040 BU0070 Homo sapiens cDNA
3221	13145	27337	1.83	4.3E-01	AA000698.1	NT	Aquifex anaerobius section 30 of 109 of the complete genome
4058	13881	27337	1.15	4.3E-01	J00308.1	NT	Human comolodactin 1 gene and flanks
4305	10351	20178	1.02	4.3E-01	AF152181.1	NT	Callitrix jacchus MWALW opsin genes, upstream flanking region
4305	10351	20179	1.02	4.3E-01	AF152181.1	NT	Callitrix jacchus MWALW opsin genes, upstream flanking region
4875	14755	27175	1.11	4.3E-01	AL161502.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 14
5058	14328	26952	1.09	4.3E-01	6638250	NT	Xenopus laevis granulosa, complete genome
5601	15514	26952	3.04	4.3E-01	AF179822.1	NT	Saccharomyces cerevisiae receptor (SSC188) gene, partial cds
6028	15533	28054	3.86	4.3E-01	AF01678.1	NT	Cornuti columni jacquica flv-g gene
6102	15980		4.01	4.3E-01	Q33307	SWISSPROT	DNA GYB3E SUBUNIT B
6350	16255		2.54	4.3E-01	AF75629.1	EST HUMAN	62020314F1 NCI CGAP-Bmr7 Homo sapiens cDNA clone IMAGE:145298 3'
6939	16787		2.83	4.3E-01	U79404.1	NT	Methanococcus voltae flagellar-related protein C1 (flaC1) genes, complete cds
7608	17458	27874	1.65	4.3E-01	AW 65900-48.1	EST HUMAN	hr74010.Y1 NCI CGAP-GUT Homo sapiens cDNA clone IMAGE:298854 5'
7608	17458	27875	1.65	4.3E-01	AW 65900-48.1	EST HUMAN	hr74010.Y1 NCI CGAP-GUT Homo sapiens cDNA clone IMAGE:298854 5'
7972	17722	27957	1.27	4.3E-01	AW 170656.1	EST HUMAN	sm69405.41 Soares, NHOC, cervical, tumor Homo sapiens cDNA clone IMAGE:2688400 3' similar to
8302	18049	20166	2.84	4.3E-01	AF075629.1	EST HUMAN	TRC000189 000189 MJ-ADAPTIN-RELATED PROTEIN 2.1
8537	18109	28673	1.98	4.3E-01	AW 96368.1	EST HUMAN	Equus caballus microsatellite LEX027
8537	18049	28674	1.98	4.3E-01	AW 963568.1	EST HUMAN	RCS-BN0034:290200-019-012 BN0034 Homo sapiens cDNA
9016	19390		2.02	4.3E-01	AJ003022.1	NT	RCS-BN0034:290200-019-012 BN0034 Homo sapiens cDNA
9616	19390		2.02	4.3E-01	AJ003022.1	NT	Streptococcus colicoides walt1 gene

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	12391	21099	1.04	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FISH HOMOLOG PRECURSOR
1904	11870		0.89	4.2E-01	AA761693.1	EST_HUMAN	mz4608.s1 NC1 CGAP GCB1 Homo sapiens cDNA clone IMAGE:128860 3'
3558	13473	22263	4.78	4.2E-01	AE030947.1	NT	Xhella testidulin, section 93 of 225 of the complete genome
3565	13469	22268	1.09	4.2E-01	AI290338.1	EST_HUMAN	gbl647.s1 S1 Soares_NFL_HIPU_S1 Homo sapiens cDNA clone IMAGE:187948 3'
3803	13715	23503	0.96	4.2E-01	AW1835527.1	EST_HUMAN	QVQ170015-180200-127-801 LT10015 Homo sapiens cDNA
3900	13810	23595	1	4.2E-01	Q04695	SWISSPROT	SOX-3 PROTEIN
4545	14438		3.63	4.2E-01	BE073574.1	EST_HUMAN	RC5-BT0559-020300-013-E06 BT0559 Homo sapiens cDNA
4598	14487	24273	4.96	4.2E-01	AA534093.1	EST_HUMAN	h19801.s1 NC1 CGAP P110 Homo sapiens cDNA clone IMAGE:397777 similar to gpM339000 HLA GLA53
4671	14557	24350	3.13	4.2E-01	R13467.1	EST_HUMAN	II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
5503	15422	24584	1.5	4.2E-01	BF242065.1	EST_HUMAN	W77471.T1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:28278 5'
5533	15490	25188	1.56	4.2E-01	AW1554182.1	EST_HUMAN	RC3-CT0264-090400-029-004 CT0264 Homo sapiens cDNA
6151	16024	26164	9.1	4.2E-01	AW158472.1	EST_HUMAN	AL158472 PLACE2 Homo sapiens cDNA clone IMAGE:200470 3'
6151	16024	26165	9.1	4.2E-01	AW158472.1	EST_HUMAN	AL158472 PLACE2 Homo sapiens cDNA clone IMAGE:200470 3'
6154	16461	26219	2.1	4.2E-01	SI25941.2	NT	Bradykinin receptor gene (beta, WF, spleen, Gastric; 419 nt, segment 2 of 2)
8217	16883	26233	5.91	4.2E-01	AL161647.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
8563	16943	26739	2.1	4.2E-01	AW167448.1	EST_HUMAN	EST358013 IMAGE resequencing, IMAGE Homo sapiens cDNA
8563	16943	26740	2.1	4.2E-01	AW167448.1	EST_HUMAN	EST358013 IMAGE resequencing, IMAGE Homo sapiens cDNA
8778	16955	26844	1.19	4.2E-01	4756039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
7692	17842	28084	1.48	4.2E-01	AW163695.1	EST_HUMAN	MF3-SN010-0200300-103-107 SN010 Homo sapiens cDNA
8400	18276	28528	2.2	4.2E-01	AB022485.1	NT	Cytosine lipase OIGC7 mRNA for membrane glyceryl cyclase, complete cds
8699	18517	28799	2.04	4.2E-01	BE059485.2	EST_HUMAN	8016603281 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3900685 3'
9803	18583		1.69	4.2E-01	AV731815.1	EST_HUMAN	RC7-BT0191-H11 Homo sapiens cDNA clone HTBB1105 5'
1078	10994	28835	1.88	4.1E-01	AI0505481.1	EST_HUMAN	RC-BT0191-210189-142 BT0191 Homo sapiens cDNA
1087	11003	28844	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAH108 5'
1087	11003	28845	2.4	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAH108 5'
1562	11496	21366	1.03	4.1E-01	AI050548.1	EST_HUMAN	RC-BT0191-210189-142 BT0191 Homo sapiens cDNA
2878	12543	22434	1.52	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2910	12936	22833	1.79	4.1E-01	AL1616362.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2910	12936	22834	1.79	4.1E-01	AL1616362.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3263	13186	22955	1.13	4.1E-01	AA003344.1	EST_HUMAN	g94008.s1 Soares_NFL_1_GBC_S1 Homo sapiens cDNA clone IMAGE:150943 3'
4177	14077	23952	2.96	4.1E-01	AI248207.1	NT	Rhodococcus sp. AD45 isoA, isoB, isoC, isoD, isoE and isoF genes
4208	14107		1.07	4.1E-01	AA003267.1	EST_HUMAN	con33402.s1 Soares_NFL_1_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'

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Table 4

Single Exon Probes Expressed in Heart

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4373	14299		0.83	4.1E-01	R41726.1	EST_HUMAN	Y511403.11 Soares infant brain cDNA clone IMAGE:31814.3'
4967	14459	24247	1.26	4.1E-01	AV747890.1	EST_HUMAN	AV747890 NPBO Homo sapiens cDNA clone NCB0210.5'
5185	15049		0.87	4.1E-01	Z99174.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3869281 to 4214814
5644	15557	20550	4.13	4.1E-01	U7887363.1	EST_HUMAN	902195590P1 NH_LMGC_83 Homo sapiens cDNA clone IMAGE:4297319.5'
6395	16237	25418	2.91	4.1E-01	U7887363.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
6983	16563	26757	1.3	4.1E-01	BF574604.1	EST_HUMAN	902133331F1 NH_LMGC_81 Homo sapiens cDNA clone IMAGE:4288238.5'
7253	17130	27323	1.23	4.1E-01	6755521	NT	Mus musculus signalling intermediate in Toll pathway evolutionarily conserved (Slbec-pending), mRNA
7888	17738		1.3	4.1E-01	AL130076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 3/3
8018	17868		1.58	4.1E-01	BF346382.1	EST_HUMAN	CV21710137-200999-010-038 HT0137 Homo sapiens cDNA
8213	18097	28349	1.64	4.1E-01	X58700.1	NT	Zea mays ZMPS2 gene for 19 kDa zinc protein
8693	17880	28121	2.79	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
9824	17022		1.72	4.1E-01	D97675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1023	18340	25783	1.27	4.0E-01	8404568	NT	Leucon tubularis mitochondrion, complete genome
1319	17223	21079	0.96	4.0E-01	AF204781.1	NT	Drosophila melanogaster: DmTubulin (dmT) mRNA, complete cds
1469	17374		1.03	4.0E-01	239833.1	NT	Mus musculus piliated derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
1590	12709	21742	1.17	4.0E-01	Z29833.1	NT	Ascaris suum msc2 gene
1650	12709	21743	1.17	4.0E-01	Z29833.1	NT	Mus musculus ubiquitin-protein ligase e3 component r-ecognin (Ubr1), mRNA
2774	10110	10331	1.09	4.0E-01	6678460	NT	Homo sapiens chromosome 21 segment HS21C080
2939	12898	22865	2.24	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2939	12898	22866	2.24	4.0E-01	AL163280.2	NT	Streptococcus pneumoniae YMC (ybc), YID (yid), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3637	13551	23339	1.61	4.0E-01	AF089803.1	NT	One atres partial J02 gene for T cell receptor delta chain (TRCDJ2), exon 1
3765	13688	23451	3.24	4.0E-01	AJ277511.1	NT	One atres partial J02 gene for T cell receptor delta chain (TRCDJ2), exon 1
3765	13688	23452	3.24	4.0E-01	AJ277511.1	NT	One atres partial J02 gene for T cell receptor delta chain (TRCDJ2), exon 1
4712	14598		7.34	4.0E-01	Q31849	SWISSPROT	NADH-PLESTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
5003	15571	25596	1.31	4.0E-01	AW070910.1	EST_HUMAN	EST382891 IMAGE: ressequences, MAGK Homo sapiens cDNA
8359	18766		3.24	4.0E-01	L76380.1	NT	Synechococcus sp. POC 9413 transposase gene, complete cds
8912	18507		2.22	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
9825	19327		1.33	4.0E-01	P30949	SWISSPROT	HYPOPHYSICAL 48.7 KD PROTEIN IN GIN2/STES INTERGENIC REGION
9910	19337		1.4	4.0E-01	AL130076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 2/6
227	10196	20207	1.99	3.9E-01	AW352188.1	EST_HUMAN	CV44110136-150959-01403 HT0136 Homo sapiens cDNA
1356	11262	21119	2.1	3.9E-01	AF208618.1	NT	Gorilla gorilla carboxy-sellar lipase (GEL) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Ttp) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2505	12473	22367	3.54	3.8E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2573	12538	22427	5.98	3.8E-01	X62032.1	NT	H. sapiens B-myb gene
2573	12538	22428	5.98	3.8E-01	X62032.1	NT	H. sapiens B-myb gene
3058	13395	22778	3.63	3.8E-01	AJ225986.1	NT	Shorthorn mab101 egf, syBz, cyd2 genes and orf3
3088	13395	23072	1.47	3.8E-01	BF502611.1	EST_HUMAN	701401.xt NIH CGAP_B18 Homo sapiens cDNA clone IMAGE:3335709 3'
4919	14798	24572	1.48	3.8E-01	BE728607.1	EST_HUMAN	001653948F NIH LMGC_20 Homo sapiens cDNA clone IMAGE:3835959 5'
5613	15528	25611	3.63	3.8E-01	BF200306.1	EST_HUMAN	001602352F NIH LMGC_59 Homo sapiens cDNA clone IMAGE:4082055 5'
7324	17200	27400	1.5	3.8E-01	AW155988.1	EST_HUMAN	X656004.xt Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR094821
7593	17372	27591	1.4	3.8E-01	A1637337.1	EST_HUMAN	w07802.xt NIH CGAP_Bm26 Homo sapiens cDNA clone IMAGE:2467658 3' similar to
7660	17390	27755	2.67	3.8E-01	M19879.1	EST_HUMAN	SW-REFX_HUMAN M4382 BINDING REGULATORY FACTOR, 1
8198	18080	27755	2.22	3.8E-01	A1605974.1	EST_HUMAN	Human clathrin 27 gene, exons 10 and 11, and L1 and Alu repeats
9297	19342	27755	2.49	3.8E-01	AF504354.1	NT	X159597.4 GBC Homo sapiens cDNA clone GBC00011 5'
9299	18340	27755	2.38	3.8E-01	CG1670	SWISSPROT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
9283	18600	28328	1.26	3.8E-01	AJ001811.1	NT	HOMEROX PROTEIN HLX1
154	10128	744	7.44	3.8E-01	AJ001811.1	NT	Thomomys maritima section 123 of 136 of the complete genome
1527	11728	22889	1.22	3.8E-01	AJ003870.1	NT	Homo sapiens protein kinase PKA beta (pkc beta), mRNA
2524	12368	22889	2.44	3.8E-01	AJ003870.1	NT	Xylem fasciculus, section 16 of 228 of the complete genome
2591	12728	22932	4.41	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYE5R-3) mRNA, complete cds
2672	12989	22732	0.92	3.8E-01	AJ251057.1	NT	Mus musculus solute carrier family 1, member 2 (SLC16A2), mRNA
3010	12938	22732	2	3.8E-01	AF043383.1	NT	Human immunodeficiency virus type 1 complete genome (isolates 9835-MP1213)
3439	13355	23100	7.77	3.8E-01	AF161516.2	NT	Plasmodium falciparum aminopeptidase N (ampN) gene, partial cds
3484	13410	23100	0.79	3.8E-01	A1607218.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3506	13410	23145	0.91	3.8E-01	A1607218.1	EST_HUMAN	w08012.xt Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3841	13752	23545	0.85	3.8E-01	6754095	NT	w08012.xt Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2357855 3'
5043	14018	24092	0.96	3.8E-01	BE544663.1	EST_HUMAN	Mus musculus general transcription factor III (GTF3), mRNA
5445	15396	24422	1.62	3.8E-01	C04888	SWISSPROT	TRANSCRIPTION FACTOR SOX-10
5904	13969	20023	4.47	3.8E-01	BE072369.1	EST_HUMAN	QV9-ET 0837-271250-046-002 BT0537 Homo sapiens cDNA clone IMAGE:3400154 5'
6953	10336	20177	3.81	3.8E-01	A1574901.1	EST_HUMAN	u05411.xt Soares, total, fetus, N264F8, 3w Homo sapiens cDNA clone IMAGE:2047917 3' similar to
6953	10336	20177	4.83	3.8E-01	A1574901.1	EST_HUMAN	contains Alu repetitive element
6980	10937	27052	3.07	3.8E-01	AB048651.1	NT	M. musculus gene for kallikrein-binding protein
							Homo sapiens mRNA for KIAA1183 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9834	19206		2.18	3.7E-01	AL121164.1	EST HUMAN	DKFZ762K076_r1 762 (synonym: hna22) Homo sapiens cDNA clone DKFZ762K076 5'
9701	19251	25217	1.52	3.7E-01	Y18900.1	NT	Homo sapiens MY2 gene
9894	19748		1.31	3.7E-01	AJ237934.1	NT	Bos taurus parafibrin-like gene, exons 2-15 and joined CDS
979	19902		7.17	3.6E-01	U89241.1	NT	Human m1p gene, partial cds
1292	11169	21054	2.59	3.6E-01	T86295.1	EST HUMAN	yc03a05.1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:24449 5'
1292	11169	21055	2.59	3.6E-01	T86295.1	EST HUMAN	yc03a05.1 Soares Infant brain IN1B Homo sapiens cDNA clone IMAGE:24449 5'
1874	11770	21945	6.05	3.6E-01	AW590184.1	EST HUMAN	hg3302.x1 NCI CGAP CG3 Homo sapiens cDNA clone IMAGE:2847419 3'
1874	11770	21945	6.05	3.6E-01	AW590184.1	EST HUMAN	hg3302.x1 NCI CGAP CG3 Homo sapiens cDNA clone IMAGE:2847419 3'
1008	11803	21682	6.18	3.6E-01	AF120207.1	NT	Mus musculus fibronectin protein S19 (Rgs19) gene, complete cds
2007	11860		1.08	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rgs11 gene
2223	12108		1.04	3.6E-01	AB002311.1	NT	Human mRNA for KIA0323 gene, partial cds
2341	12221		2.39	3.6E-01	X76725.1	NT	P. f. irregular (P3804) gene for actin
2437	12314	22211	1.63	3.6E-01	AW182033.1	EST HUMAN	RG3-ST0171-11036-01-c07 ST0171 Homo sapiens cDNA
2890	12460	22360	2.28	3.6E-01	P24208	SWISSPROT	PROTEIN ISOSPARTATE O-METHYLTRANSFERASE (PROTEIN BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2890	13077		0.9	3.6E-01	AF169463.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3424	13341	23145	1.85	3.6E-01	X76753.1	NT	H. sapiens serolectin transporter gene, exons 9 and 10
3424	13341	23146	1.85	3.6E-01	X76753.1	NT	H. sapiens serolectin transporter gene, exons 9 and 10
4308	14205	23698	1.16	3.6E-01	U677683.1	EST HUMAN	RC1-H10545-10000-01-14-B12 H10545 Homo sapiens cDNA
4633	14323	24312	0.83	3.6E-01	AJ209699.1	NT	Bacillus thuringiensis mRNA for MAPK alpha subunit protein
4684	14570	24397	1.23	3.6E-01	AJ23237.1	NT	Bacteria from anoxic bulk soil 10S rRNA gene (strain XB48)
4841	14619	24597	2.01	3.6E-01	AW336933.1	EST HUMAN	h02g01.x1 NCI CGAP Luc4 Homo sapiens cDNA clone IMAGE:2872966 3'
5959	15805	25928	1.0	3.6E-01	Y101936.1	NT	Homo sapiens PHEX gene
6235	19104		6.49	3.6E-01	R64909.1	EST HUMAN	w74d01.1 Soares fetal liver spleen TNFSF15 Homo sapiens cDNA clone IMAGE:276887 5'
6317	19160	26340	1.69	3.6E-01	AW027174.1	EST HUMAN	w72c10.1 Soares, thymus, NF1H7 Homo sapiens cDNA clone IMAGE:2813010 3' similar to TR-O16117
6819	19995	26886	13.42	3.6E-01	AL167983.2	NT	O15117 PYB BINDING PROTEIN, [P1]; Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
7205	17052	27299	3.37	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7205	17052	27270	3.37	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7302	17178	27380	1.4	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS212004
7674	17324	27750	15.34	3.6E-01	Q93194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y475

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8314	18191	28440	1.94	3.6E-01	BE002690.1	EST_HUMAN	981670416F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:586987 5'
8453	18326	28895	3.99	3.9E-01	AE004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
8741	17860	28134	3.56	3.6E-01	AE000886.1	NT	Methanobacterium thermoautotrophicum from basins 702375 to 714311 (section 62 of 148) of the complete genome
6044	18761	18761	1.81	3.6E-01	Y18210.1	NT	Homo sapiens NRH8 gene for hair keratin, exons 1 to 9
9127	18886		3.03	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1355 section 225 of 400 of the complete genome
9281	18933		3.03	3.6E-01	U69888.1	NT	Mus musculus Emr1 mRNA, complete cds
9889	19704		1.58	3.6E-01	AW190229.1	EST_HUMAN	X60611.1 x1 NC1 CGAP_Pam1 Homo sapiens cDNA clone IMAGE:2578116 3' similar to gbK00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
992	10174	16090	2.18	3.6E-01	6578623	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
992	10566	20414	0.97	3.6E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 71
708	10940	20469	1.24	3.6E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	13640	20467	1.24	3.6E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
708	10934	20591	3.17	3.9E-01	BF130766.1	EST_HUMAN	90181008R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4083951 3'
1603	11508	21370	1.17	3.9E-01	BF10668.1	EST_HUMAN	90189468R2 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4142444 5'
1622	11526	21384	1.05	3.9E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2663	12725	22327	1.85	3.9E-01	AA22252.1	EST_HUMAN	2028409.1 Statagene NT2 neuronal precursor 837200 Homo sapiens cDNA clone IMAGE:659872 3'
2672	12937		0.86	3.9E-01	U05987.1	NT	Fluoribacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
4165	14095	23839	1.92	3.9E-01	AF071283.1	NT	Danio rerio homodimer protein (hmd550) gene, complete cds
4979	14275	24059	1.29	3.9E-01	BE146595.1	EST_HUMAN	RCH-F10218-181069-011-g02-H10218 Homo sapiens cDNA
4760	14975	24492	0.84	3.9E-01	N81203.1	EST_HUMAN	7885ET total brain cDNA Homo sapiens cDNA clone 7885ET-X similar to R07870, 240468
4849	14730	24513	3.84	3.9E-01	MT8349.1	NT	Rat leukocyte common antigen (LCA) gene, exons 1 through 3
6190	15939		3.47	3.9E-01	U08006.1	NT	Sacchara mRNA for CD31 protein (PECAM-1);
6704	16584	1686	1.88	3.9E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7171	17048	27238	3.21	3.9E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
7912	17463	27890	1.51	3.9E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL II) (981)
7888	17538	27764	2.99	3.9E-01	Z29825.1	NT	Xenopus rhodopsin gene for opsin protein
8116	18005	28261	2.99	3.9E-01	AF10084.1	NT	C. parvulus rhodopsin gene for opsin protein
8386	18233	28513	2.34	3.9E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8386	18233	28514	2.34	3.9E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8951	18758	20052	3.34	3.4E-01	AL161901.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
9206	19337		2.12	3.4E-01	XK4565.1	NT	B. taurus alpha 1 gene for F10F(1) ATP synthase alpha-subunit
9847	19316	24669	2.25	3.4E-01	H80914.1	EST HUMAN	ye4H11.1 Sources retina N204HR Homo sapiens cDNA clone IMAGE:210697 5'
9941	19316	25000	2.25	3.4E-01	H80914.1	EST HUMAN	ye4H11.1 Sources retina N204HR Homo sapiens cDNA clone IMAGE:210697 5'
991	19324		1.9	3.4E-01	AL242956.1	NT	Homo sapiens partial N-myc (exam 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
990	19383	20731	4.53	3.4E-01	Y07938.2	NT	Pseudomonas fluorescens cofR, cds genes, o7222 and partial lncA gene
1304	11211	21066	1.73	3.4E-01	Y00554.1	NT	Azobacter vinelandii nifA gene for NifA protein (cofixase regulatory element)
2852	12232	22129	2.81	3.4E-01	D60009.1	NT	Synechococcus sp. PCC6803 complete genome, 11/27, 1317235-1430418
2842	12509	22400	1.48	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2971	12886	22697	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2971	12886	22698	0.81	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3124	13049	22848	5.41	3.4E-01	U83005.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGB1) mRNA, complete cds
3468	13404	23200	3.46	3.4E-01	AF108383.1	NT	Methylobacter sp. strain SSI putative GpE (gptE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3722	13834		2.38	3.4E-01	BF448010.1	EST HUMAN	TRIM49.1 x1 NC1_CGAP_Ov16 Homo sapiens cDNA clone IMAGE:3872232.3 similar to TRIM49.16
3965	13872		1.16	3.4E-01	AA594196.1	EST HUMAN	330U13.DJ1063.11
4394	14280	24074	0.78	3.4E-01	AF186341.1	NT	hori1010.31 NC1_CGAP_Phr1 Homo sapiens cDNA clone IMAGE:1100347.3
4544	14437	24221	1.82	3.4E-01	BE009012.1	EST HUMAN	Homo sapiens integrin alpha 6 (ITGA6) genes, exons 12 through 23
4626	14710	24494	0.93	3.4E-01	BE463761.1	EST HUMAN	h1y7609.41 NC1_CGAP_G035 Homo sapiens cDNA clone IMAGE:3197985.3 similar to contains L17B L1 repetitive element
4670	14790		3.57	3.4E-01	AB240973.1	EST HUMAN	gip505.41 NC1_CGAP_K163 Homo sapiens cDNA clone IMAGE:1807208.9 similar to contains Alu repetitive element
4870	14845	24614	1.2	3.4E-01	X118644.1	NT	Sea urchin hsp70 genes II for heat shock protein 70
5487	15406	25469	2.85	3.4E-01	AF161594.2	EST HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5591	15467		4.71	3.4E-01	AA080313.1	EST HUMAN	zn12011.41 Striatum HNT neuron (R637233) Homo sapiens cDNA clone IMAGE:547221.3'
5954	15566	25724	2.06	3.4E-01	L03971.1	NT	Ecdyotus 22 1AB, 1C, 2A, 2B, 2C, 3A, 3B, 3C, 3D protein RNA, complete mature peptides and cds
5715	15923	25724	2.57	3.4E-01	AW204505.1	EST HUMAN	U-HH11-see-e-12-GUJ1.31 NC1_CGAP_Su43 Homo sapiens cDNA clone IMAGE:2719582.3'
5780	15987	25769	1.47	3.4E-01	AL120544.1	EST HUMAN	DIC-Zp76761A249_1 791 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:2719582.3'
6045	15948		1.52	3.4E-01	N95226.1	EST HUMAN	p553er12.51 Sources_fetal_Lung_NHL161W Homo sapiens cDNA clone IMAGE:307342.3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6148	10021	20161	1.41	3.4E-01	AI488082.1	EST HUMAN	trnS905 t ¹ NC, CGAP Brn23 Homo sapiens cDNA clone MA6G:2102940 3' similar to gbS37481
6943	16621		1.77	3.4E-01	A4337003.1	EST HUMAN	LAMININ RECEPTOR (HUMAN);
7130	17709	27209	1.62	3.4E-01	9633924	EST HUMAN	EST147708 Endometrial tumor Homo sapiens cDNA 5' end
7313	17189	27390	3.88	3.4E-01	P20013	SWISSPROT	Bovine enterovirus strain K2317, complete genome
7313	17189	27391	3.88	3.4E-01	P20513	SWISSPROT	INTEGRIN BETA-3 PRECURSOR
7433	19446	28036	4.17	3.4E-01	U19402.1	SWISSPROT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7433	19446	28036	4.17	3.4E-01	U19402.1	SWISSPROT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7600	17540	27166	2.22	3.4E-01	A222084.1	NT	Homo sapiens PAA genes, exon 16, 17 and 18
8380	18237		4.09	3.4E-01	AEC030891.1	NT	Melanoblastic Thermococcus thermophilus from bases 1018444 to 1022212 (section 87 of 148) of the complete genome
8407	18263	28556	2.2	3.4E-01	P09525	SWISSPROT	PROBABLE E4 PROTEIN
8440	18814	28672	2.20	3.4E-01	AF045981.1	NT	Radial acetyl cytochrome b (cytb) genes, mitochondrial gene encoding mitochondrial protein, partial cds
8604	18471	28742	1.77	3.4E-01	P20366.1	NT	Human von Willebrand factor gene, exons 30 and 37
8604	18471	28743	1.77	3.4E-01	P20366.1	NT	Human von Willebrand factor gene, exons 30 and 37
8700	18805	28895	1.8	3.4E-01	M093507.1	NT	Rattus norvegicus mRNA for s-gliadin/LC18, complete cds
8814	19827	28616	4.03	3.4E-01	AL161615.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment NC_27
8820	18814		2.01	3.4E-01	U93004.1	NT	Citrus variegation virus putative replicase gene, partial cds
9130	18887		1.3	3.4E-01	Z21621.1	NT	Saccharomyces cerevisiae Riboflavin synthase
9220	19038		1.82	3.4E-01	AF259435.1	NT	Schistosoma haematophysete pombe Riboflavin synthase
9347	19024		4.9	3.4E-01	L26339.1	NT	Human autologous mRNA, complete cds
9378	19539		2.40	3.4E-01	BE216682.1	EST HUMAN	hym208 t ¹ NC, CGAP U024 Homo sapiens cDNA clone MA6C:3176127 3' similar to contains PTR5.18
9432	18039		2.13	3.4E-01	9638861	NT	PT55 repetitive element;
9537	19740	25264	1.79	3.4E-01	AJ287191.1	NT	Saccharomyces cerevisiae, complete genome
9829	19930		1.78	3.4E-01	AF010413.1	NT	Mus musculus S1L, MAP_17, CYP_3, SGL_5, CYP_5 genes
14	10000	19791	7.61	3.8E-01	X07390.1	NT	Homo sapiens HLA class III region containing tetranin X (tetranin-X) gene, partial cds, cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, halsase (SK2W), RO complement factor B (Bf), and complement component C2 (C2) genes;>
100	10091	19791	1.90	3.8E-01	X07390.1	NT	Rhizobium leguminosarum sym plasmid pRL51/ nodX gene
440	10384	20208	1.16	3.3E-01	AF115453.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment NC_45
617	10505	20366	1.41	3.3E-01	7682485	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment NC_45
1182	11063	20540	3.05	3.3E-01	Q12449	SWISSPROT	HOMO PROLINE-RICH PROTEIN (KAA1100), mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1285	11193	21046	4.82	3.9E-01	BF56980.1	EST_HUMAN	60214016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:300251 3'
1588	11462	21352	1.11	3.9E-01	6753682	NT	Mus musculus desintegrin 5' (Digs5), mRNA
1704	11605		1.05	3.3E-01	AA32734.1	EST_HUMAN	EST:591722 Homo sapiens cDNA 5' end
							Homo sapiens uridine monophosphate synthetase (uridine phosphorylase), transferase and orotidine-5'- decarboxylase (UMPS) mRNA
2355	12235		4.74	3.9E-01	4607834	NT	Bacteriophage phi-Yeo3-12 complete genome
2319	12846	22946	2	3.3E-01	AJ251805.1	NT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
2682	12910	22737	1.12	3.9E-01	002743	SWISSPROT	Streptomyces griseolatus mitochondrial biosynthetic genes
3018	12941	22737	1.01	3.9E-01	AJ007632.2	NT	Homo sapiens MTA-1-L1 gene, complete cds
3459	13957	24173	1.14	3.9E-01	AB012922.1	NT	EXOXYTRIPONUCLEASE V BETA CHAIN
3748	13950	23433	2.17	3.9E-01	Q64945	SWISSPROT	Xanthopsylla thalassia DNA chromosome 4, contig fragment No. 10
3884	13795	22682	1.59	3.9E-01	AI161488.2	NT	Hypocodon fragiforme chitin synthase gene, partial cds
3920	13829	22609	1.92	3.9E-01	AF203448.1	NT	Hydroxymethylglutaryl-CoA lyase, partial cds
4271	14170		2.74	3.9E-01	D31692.1	NT	Rattus norvegicus DNA for neurexin, partial cds
4589	14477		1.46	3.9E-01	AJ539114.1	EST_HUMAN	h978912.1 NCI_CGAP_US Homo sapiens cDNA clone IMAGE:2205407 3' similar to gi:557522 ANTIGEN PEPTIDE: TPASPORTER 1 (HUMAN)
5263	15185	24680	2.08	3.9E-01	X63619.1	NT	R. congoensis mRNA for 3UTR of ubiquitin-like protein
5293	16185	24681	2.68	3.9E-01	X63619.1	NT	R. congoensis mRNA for 3UTR of ubiquitin-like protein
5622	16537	25623	2.71	3.9E-01	BE616560.1	EST_HUMAN	6014722681T NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3815753 3'
5622	16537	25624	2.71	3.9E-01	BE616560.1	EST_HUMAN	6014722681T NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3815753 3'
6117	16011	26148	3.64	3.9E-01	AJ628131.1	EST_HUMAN	y64601.x1 NCI_CGAP_HK111 Homo sapiens cDNA clone IMAGE:2285609 3' similar to contains AU repetitive element/contains element L1 repetitive element;
6117	16011	26149	3.64	3.9E-01	AJ628131.1	EST_HUMAN	y64601.x1 NCI_CGAP_HK111 Homo sapiens cDNA clone IMAGE:2285609 3' similar to contains AU repetitive element/contains element L1 repetitive element;
6676	16433	26616	1.5	3.9E-01	N85146.1	EST_HUMAN	J2468F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2468 5' similar to TEGT
6981	16838	27059	19.48	3.9E-01	BF693654.1	EST_HUMAN	6021403271T NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301900 5'
7477	17337	27542	3.26	3.9E-01	N93966.1	EST_HUMAN	zaf7101 a1 Soares, fetal lung, NHL 19W Homo sapiens cDNA clone IMAGE:287949 3'
7507	17295	27504	2.81	3.9E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250600-011-g14 TN0077 Homo sapiens cDNA
7739	17659		2.07	3.9E-01	L14044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG-C) gene, exons 1-3, complete cds
8104	17004	28242	2.71	3.9E-01	X63953.1	NT	Drosophila Adh gene
8104	17094	28243	2.71	3.9E-01	X63953.1	NT	Drosophila Adh gene
8389	18235		1.82	3.9E-01	BF526469.1	EST_HUMAN	902070502F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:421558 5'
8561	18431	28700	12.76	3.9E-01	BE216891.1	EST_HUMAN	h951902.x1 NCI_CGAP_L424 Homo sapiens cDNA clone IMAGE:3175978 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8652	18541	28825	3.94	3.3E-01	P47693	SWISSPROT	GALACTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
8655	18763		4.79	3.3E-01	AA090321.1	EST_HUMAN	db*1602-11 NQ1_OGAP CBP1 Homo sapiens cDNA clone IMAGE:1338930
8672	10000	10791	1.89	3.3E-01	X07590.1	NT	Rhizobium leguminosarum sym plasmid pRL6J1 nodX gene
9119	18881	28789	1.63	3.3E-01	6598316	NT	Homo sapiens aldolase oxidase 1 (AOX1), mRNA
9817	18323		0.05	3.3E-01	AF000002.1	NT	Protophysa horridicola OTS genomic DNA, 28701-54000 nt, position 127
449	10393		1.98	3.2E-01	AL161291.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
701	10334		2.05	3.2E-01	AL161291.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87
1149	11059	20602	18.98	3.2E-01	AF047013.1	NT	Fusarium roseum virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1261	11199	21019	1.04	3.2E-01	Z50232.1	NT	P. vulgata ar5-1 gene
1369	11274	21130	0.25	3.2E-01	Q46924	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1737	11838	21503	1.22	3.2E-01	Z39041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172p
1744	11945	21515	0.3	3.2E-01	AY029104.1	EST_HUMAN	EST1592854 IMAGE repository, MACD Homo sapiens cDNA
1744	11945	21514	3.5	3.2E-01	AY029104.1	EST_HUMAN	EST1592854 IMAGE repository, MACD Homo sapiens cDNA
1800	11988	21574	1.18	3.2E-01	AF111055.1	NT	Bovine chaperonin 14 kDa cDNA library under conditions of nitrogen deprivation
2114	12003	21901	2.89	3.2E-01	BF203871.1	EST_HUMAN	001668604F NIH_MGC-17 Homo sapiens cDNA clone IMAGE:411512 5'
2494	12358		2.9	3.2E-01	7710079	NT	Mus musculus Ptdinotectin 1 homobox (Ptdinot), mRNA
2577	12542	22433	1.55	3.2E-01	AF000598.1	NT	Homo sapiens trypsinogen-like zymogen zymogen (PLZP) gene, complete cds
3555	13470		0.96	3.2E-01	D10872.1	NT	Human hNAT allele 5.2 gene for arylamine N-acetyltransferase
3695	13779		0.97	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
4295	14193	23977	1.35	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4375	14271	24052	0.81	3.2E-01	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cros gene, complete cds; and unknown gene
4397	14293	24077	1.33	3.2E-01	Q10298	SWISSPROT	HYPOHEMATIC 91.7 KD PROTEIN C19G7.04C IN CHROMOSOME 1 PRECURSOR
4832	14320		5.86	3.2E-01	BF030671.1	EST_HUMAN	392081672F NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
4807	15081		1.18	3.2E-01	M32352.1	NT	Mouse resin (Ren-1-c) gene, complete cds
5133	15000	24771	0.98	3.2E-01	AY009847.1	NT	Homo sapiens Interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5233	15145	24913	2.82	3.2E-01	BE173964.1	EST_HUMAN	CACD-H10509-000300-239-110 H10509 Homo sapiens cDNA
6752	19331	28819	1.42	3.2E-01	M60266.1	NT	Rat ISO-nitric reductase factor gene, complete cds
5872	16751	20945	13.32	3.2E-01	X02508.1	NT	Homo sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
5875	16754	20951	14.29	3.2E-01	BF031035.1	EST_HUMAN	392081672F NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4129533 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6929	19807		1.35	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
6986	19803	27096	1.5	3.2E-01	AE002015.1	NT	Dennouose radicle R1 section 152 of 229 of the complete chromosome 1
7247	17124		2.19	3.2E-01	ME8511.1	NT	Homo monkey antigen CD14 (CD14) mRNA, complete cds
7741	17591	27812	3	3.2E-01	U44974.1	NT	Borrelia burgdorferi plasmid sp2.2, <i>erpC</i> and <i>erpD</i> genes, complete cds, and unknown genes
7910	17760		3.25	3.2E-01	AA011359.1	NT	Homo sapiens gene for AF-5, complete cds
8058	17949	26199	2.7	3.2E-01	T06813.1	EST HUMAN	EST04702 Fetal brain, <i>Stratigine</i> (cath63535) Homo sapiens cDNA clone HF8D221
8152	19862		3.28	3.2E-01	L07288.1	NT	<i>Drosophila melanogaster</i> laminin A (Lam-A) mRNA, complete cds
8665	16226		2.97	3.2E-01	Q63217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
8801	19313		1.58	3.2E-01	L38874.1	NT	Homo sapiens deoxyxylate deaminase gene, complete cds
8855	19866	24698	1.57	3.2E-01	BE388776.1	EST HUMAN	60127480FT NIH MGCC 20 Homo sapiens cDNA clone IMAGE:3618748 5'
2636	12503	22937	3.73	3.1E-01	R19031.1	EST HUMAN	949D98.1 Soares fetal liver setten 1NRLS Homo sapiens cDNA clone IMAGE:126051 5' similar to gb:546241 OM PROTEIN (HUMAN);
2693	12855	22419	3.45	3.1E-01	7651971	NT	Homo sapiens KIA00174 gene product (KIA00174), mRNA
2695	12855	22420	3.45	3.1E-01	7651971	NT	Homo sapiens KIA00174 gene product (KIA00174), mRNA
2827	12758		4.01	3.1E-01	AW52009.1	EST HUMAN	h48R03.3 Soares, NR_1, GBC 3.1 Homo sapiens cDNA clone IMAGE:2975391 3'
3155	13091	23536	2.78	3.1E-01	AA023693.1	NT	Man musculus gene for Sirt1/Trk kinase KXJMBE, exon 8
3832	13744	24717	1.15	3.1E-01	AJ251565.1	NT	Quacae carolinensis mRNA for transcription factor ERF (ERF gene)
5073	14943	24717	0.89	3.1E-01	AA075308.1	EST HUMAN	hmd11003.1 NC_1, COMP_B13 Homo sapiens cDNA clone IMAGE:1072161 3'
5447	15265	25119	8.68	3.1E-01	AF171911.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF-3A) gene, exon 1
5527	15444	26510	45.03	3.1E-01	Y15278.1	NT	Man musculus mRNA for polyoma
5590	19796	24951	1.94	3.1E-01	AF184122.1	EST HUMAN	Homo sapiens laminin 2 (HLN2) gene, exons 10 through 22
6160	19438	26818	1.34	3.1E-01	AF168360.1	EST HUMAN	RC3-HN0001-31030303H1-H04 HN0001 Homo sapiens cDNA
7023	19800	27092	2.4	3.1E-01	BF737692.1	EST HUMAN	93004121FT NIH MGCC 30 Homo sapiens cDNA clone IMAGE:5604420 5'
7791	17841	27874	7.76	3.1E-01	R44518.1	EST HUMAN	949R04.1 Soares infant brain NIH Homo sapiens cDNA clone IMAGE:36939 3'
7791	17841	27874	7.76	3.1E-01	BF696899.1	EST HUMAN	90212474FT NIH MGCC 56 Homo sapiens cDNA clone IMAGE:4281611 5'
7832	17882	27926	1.96	3.1E-01	AJ244001.1	EST HUMAN	961et1.x1 NC1, CGAP MG8 Homo sapiens cDNA clone IMAGE:1693980 3' similar to gb:555700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
8221	18055	28346	1.95	3.1E-01	BF221117.1	EST HUMAN	90188552FT NIH MGCC 57 Homo sapiens cDNA clone IMAGE:005814 5'
8231	19336	28920	1.99	3.1E-01	7652291	NT	Homo sapiens KIA00764 gene product (KIA00764), mRNA
9279	18882		1.83	3.1E-01	AF294008.1	NT	Anolis opalinus nucleotide QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial protein
9315	19007		1.64	3.1E-01	AF304162.1	NT	Stizocodon vitreum 40S ribosomal protein S11 mRNA, partial cds
9457	19089		2.45	3.1E-01	AF196959.1	EST HUMAN	Homo sapiens membrane-bound aminopeptidase P (ANPEP2) gene, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9805	18318		3.11	3.1E-01	AF198779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, TS4 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α -
66	12935	19868	1.56	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Ple), mRNA
254	10220	20037	11.12	3.0E-01	AJ277735.1	NT	Homo sapiens Xq pseudobacterial region; segment 1/2
1204	11114	20960	1.89	3.0E-01	AW300400.1	EST HUMAN	hcd3068.x1 NC1 CGAP JGdH1 Homo sapiens cDNA clone IMAGE:2774343 3'
1497	11395	21256	6.26	3.0E-01	AJ006755.1	NT	Balanophora physalis gene encoding atypical natriuretic peptide
2089	11976	21873	0.89	3.0E-01	AF237778.1	NT	Rattus norvegicus Cdc2/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3175	13100		0.98	3.0E-01	AF030461.1	NT	Corynebacterium sp. ALV-1 α -NPG gene for polyphosphate kinase, complete cds
3769	13701	23488	1.34	3.0E-01	AW817785.1	EST HUMAN	PM1-S10262-261100-001-901 STC292 Homo sapiens cDNA
4412	14308	24059	1.91	3.0E-01	AJ007563.1	NT	Balanophora physalis gene encoding atypical natriuretic peptide
5283	15205	24891	5.34	3.0E-01	BE741698.1	EST HUMAN	R0159490F1 NIH MG3C-9 Homo sapiens cDNA clone IMAGE:3948734 5'
5578	15206	25147	3.18	3.0E-01	BE65576.1	EST HUMAN	RC3-B10333-160700-111-403 B10333 Homo sapiens cDNA
5579	15206	25146	3.18	3.0E-01	BE65576.1	EST HUMAN	RC3-B10333-160700-111-403 B10333 Homo sapiens cDNA
5601	15320	25368	3.51	3.0E-01	U012473.1	NT	Mus musculus 129ev Clara cell 10 kD protein (mGCT10) gene, complete cds
5606	15320	25371	2.61	3.0E-01	D18313.1	NT	Mus musculus 129ev Clara cell 10 kD protein (mGCT10) gene, complete cds
5635	15366	25388	2.57	3.0E-01	16047007	NT	Mus musculus midbrain (Midi-protid), mRNA
6429	15260	25451	1.35	3.0E-01	AF0071810.1	NT	Streptococcus pneumoniae strain DBS3 Paga (Paga) gene, partial cds
6525	15505	25693	1.25	3.0E-01	AF007185.1	NT	Thermoplasma maritima section 07 of 139 of the complete genome
6677	16766		4.87	3.0E-01	6910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec4e), mRNA
6697	16815	27007	1.27	3.0E-01	BE560683.1	EST HUMAN	R0153007F1 NIH MG3C-53 Homo sapiens cDNA clone IMAGE:5861594 5'
7544	17794	26034	1.86	3.0E-01	AF090231.1	NT	Aspergillus oryzae BipA gene for ER chaperone Bip, complete cds
8860	18785	29074	2.86	3.0E-01	H101026.1	EST HUMAN	y84b10.17 Scores full liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194707 5'
8860	18785	29075	2.89	3.0E-01	H101026.1	EST HUMAN	y84b10.17 Scores full liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194707 5'
9854	19847		1.43	3.0E-01	AJ297831.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
9858	19900		2.76	3.0E-01	6977760	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA), mRNA
1878	11871	21762	1.6	2.8E-01	AE2000736.1	NT	Aquileae scutellum section 08 of 109 of the complete genome
2207	12068	21869	0.96	2.8E-01	AF222718.1	NT	Chyrodolymus syntrophic mitochondrion, complete genome
3147	13072	22873	1.03	2.8E-01	AF075911.1	NT	Xenopus laevis transcription factor E2F, mRNA, complete cds
3213	13137	22939	2.26	2.8E-01	AW1754239.1	EST HUMAN	PM1-C70326-171299-001-F12 C70326 Homo sapiens cDNA
3213	13137	22940	2.26	2.8E-01	AW1754239.1	EST HUMAN	PM1-C70326-171299-001-F12 C70326 Homo sapiens cDNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
596	10497		1.84	2.9E-01	U67139.1	NT	Rattus norvegicus A-linase anchoring protein AKAP140 mRNA, complete cds
1067	10693	20328	2.47	2.8E-01	AF169050.1	NT	Gula gila oocyte maturation factor Mos (c-mos) gene, partial cds
1256	11183	21013	1.1	2.8E-01	BE313442.1	EST_HUMAN	BT1146733F1 NH1.MGC_19 Homo sapiens cDNA clone IMAGE:316388 5'
1266	11183	21014	1.1	2.8E-01	BE313442.1	EST_HUMAN	BT1146733F1 NH1.MGC_19 Homo sapiens cDNA clone IMAGE:316388 5'
1269	11179	21025	1.01	2.8E-01	D99560.1	NT	Human mRNA for sarin/threonine protein kinase, complete cds
1596	11568	21470	1.55	2.8E-01	AV159020.1	EST_HUMAN	QY1-210394-120203-005-05 CT0384 Homo sapiens cDNA
1696	11860	21750	1.77	2.8E-01	AL047620.1	EST_HUMAN	DKFZ56902321.J1 538 (synonym: hua1) Homo sapiens cDNA clone DKFZ56902321
2094	11974	21969	1.47	2.8E-01	AV151185.1	EST_HUMAN	h44403.x1 Scores: NFWL_T: G93C_S1 Homo sapiens cDNA clone IMAGE:2512333 3'
2423	12300	22107	2.94	2.8E-01	AE000484.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2423	12300	22198	2.94	2.8E-01	AE000484.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2500	12375		2.47	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4 contig fragment No. 65
2830	12498	22338	1.97	2.8E-01	AE020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
3940	13697		1.49	2.8E-01	AF172480.1	NT	Tetrahymena gonidi 500Qa heat-shock protein (HS500) mRNA, partial cds
3941	13698	22627	2.48	2.8E-01	Z14037.1	NT	B.aurus microsatellite (ETH121)
3941	13698	22628	2.48	2.8E-01	Z14037.1	NT	B.aurus microsatellite (ETH121)
3332	13262	23057	1.1	2.8E-01	AF000044.1	NT	Pyrococcus horikoshii OT3 genome: DNA, 771001-584900 nt, position (47)
3915	13624	23604	1.78	2.8E-01	AE01180.1	NT	Borrelia burgdorferi (strain 05 of 70) of the complete genome
4103	14003		2.21	2.8E-01	AI096668.1	EST_HUMAN	ov4910.x1 Scores: NFWL_T: Homo sapiens cDNA clone IMAGE:1642226 3' similar to contains Alu repetitive element/contains element MER22 repetitive element
4352	14248	24034	0.98	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contig; putative Magad genes, Caltracin, MUP(P) steroid dehydrogenase and Zinc finger protein 165
4357	14283	24038	2.2	2.8E-01	PI13615	SWISSPROT	HNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4673	14569	24362	1.03	2.8E-01	D16050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4673	14569	24363	1.03	2.8E-01	D16050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4722	14908	24394	2.8	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4785	14940	24427	1.54	2.8E-01	BF328183.1	EST_HUMAN	g02042001F1 NC1.CGAP_Bmg7 Homo sapiens cDNA clone IMAGE:1810129 5'
4787	14672	24459	1.7	2.8E-01	AI272696.1	EST_HUMAN	g02042001F1 NC1.CGAP_Bmg7 Homo sapiens cDNA clone IMAGE:1810129 5'
5252	15440	24948	21.36	2.8E-01	AA3166697.1	EST_HUMAN	repetitive element/contains element LTR repetitive element
5143	15363	25419	2.33	2.8E-01	AB0166025.1	NT	Homo sapiens OCTN2 gene, complete cds
5770	16577	25794	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
5770	16577	25795	1.44	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
6038	15941	26073	7.67	2.8E-01	BF511215.1	EST_HUMAN	U1H-B4-af-04-04-U1.s1 NC1.CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085162 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6713	16893	26791	1.24	2.8E-01	A346126.1	EST_HUMAN	qp-4801.x1 NCL CGAP_CoII Homo sapiens cDNA clone IMAGE:190289 3' similar to gp-X06323_cds1
6713	16893	26762	1.24	2.8E-01	A46168.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
6776	16857	26847	2.39	2.8E-01	U71688.1	EST_HUMAN	qp-4801.x1 NCL CGAP_CoII Homo sapiens cDNA clone IMAGE:190289 3' similar to gp-X06323_cds1
6994	16871	27388	7.25	2.8E-01	BF347847.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
7311	17187	27388	1.35	2.8E-01	AF080502.1	EST_HUMAN	6C2022687FT NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4758628 5'
7900	17451		1.15	2.8E-01	L13954.1	NT	Mus musculus centrin (Cent2) gene, complete cds
7786	17639	27872	2.79	2.8E-01	7706163	NT	Lycopodium esculentum peroxidase (TPX1) mRNA
8126	18074	28251	2.27	2.8E-01	BF241062.1	EST_HUMAN	Homo sapiens hypophosphidic protein (LOC31319), mRNA
8126	18074	28252	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880754FT NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8183	18041	28231	3.01	2.8E-01	BF959570.1	EST_HUMAN	601880754FT NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8254	18134	28382	2.62	2.8E-01	AF051662.1	NT	601852148FT NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4076028 5'
8592	18466		3.49	2.8E-01	BF570225.1	EST_HUMAN	Drosophila heterocerus fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
9562	19160		0.37	2.8E-01	CE33293.1	NT	60213147FT NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4273833 5'
9567	19210	28236	3.11	2.8E-01	BE778693.1	EST_HUMAN	Mus musculus DNA for preproinsulin D2 synthesis, complete cds
9628	19551		0.89	2.8E-01	11436226	NT	PM4-H10951630000-001-487 H109516 Homo sapiens cDNA
405	10411	20230	2.33	2.7E-01	Y17324.1	NT	Homo sapiens CDG12-binding protein kinase beta (DMPK-beta) (CDG423P9), mRNA
597	10333		3.14	2.7E-01	AA450061.1	EST_HUMAN	Rattus norvegicus CDG12B mRNA
1240	11747	20996	1.49	2.7E-01	A5004006.1	NT	263910.1 Scores, total, Jukes, N62HF9, 9w Homo sapiens cDNA clone IMAGE:78827 3' similar to
1504	11500		1.73	2.7E-01	X79816.1	NT	contains AU repetitive element;
1698	11609	21471	2.96	2.7E-01	W90667.1	EST_HUMAN	homo sapiens transposable element Tc100 gene for transposase, complete cds
1739	11639	21507	1.25	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P1; 2; CORE PROTEIN P1; 6; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2089	12712		2.38	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2316	12167	22094	8.78	2.7E-01	Y13988.1	NT	Feline immunodeficiency virus env gene, isolate ITTO088PU (M89), partial
2406	12283	22180	3.61	2.7E-01	A310866.1	EST_HUMAN	ts43511.x2 NCL CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046938 3' similar to contains element L1
2959	12833		1.25	2.7E-01	BF085264.1	EST_HUMAN	repetitive element;
3029	13618	23618	1.88	2.7E-01	AF026191.1	EST_HUMAN	GM7-H0875-060900-385-c05 H0875 Homo sapiens cDNA
3043	13851	23626	2.31	2.7E-01	Y17569.1	NT	wa52a11.x1 NCL CGAP_K011 Homo sapiens cDNA clone IMAGE:2462828 3'
4766	14681	24468	0.89	2.7E-01	L27616.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
							Trilicium aestivum (Wcs60) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Ht BLAST E Value	Top Ht Accession No.	Top Hit Database Source	Top Hit Descriptor
4973	14848		3.5	2.7E-01	AF056131.1	EST_HUMAN	
5221	15144	24888	3.49	2.7E-01	P17277	SWISSPROT	RC1-OT0296-200200-016-003 CT0288 Homo sapiens cDNA
6064	10047	26192	2.25	2.7E-01	Q01554	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (HOXA-1-4)
6527	10366	26595	2.23	2.7E-01	AF24054.1	NT	FIBRILLIN 1 PRECURSOR
6527	10366	26595	2.23	2.7E-01	AF24054.1	NT	Bos taurus intronless calcium activated neutral protease 1 (CAPN-1) gene, exons 11-20, and partial cds
7378	17247	27453	10.09	2.7E-01	Q83909	SWISSPROT	Bos taurus intronless calcium activated neutral protease 1 (CAPN-1) gene, exons 11-20, and partial cds
7378	17247	27454	10.09	2.7E-01	Q83909	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7378	17248		2.24	2.7E-01	P37928	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7801	17651	27888	1.29	2.7E-01	AF091848.1	NT	FNBR1A2 W PROTEIN
7827	17677	27921	1.93	2.7E-01	AF091848.1	NT	Cyclodextrin cyclase calgranulin G mRNA, partial cds
8187	18073	28322	1.76	2.7E-01	AF059043.1	EST_HUMAN	Mus musculus transcription factor NF-ATc1 isoform a (NF-ATc1) mRNA, complete cds
8187	18073	28323	1.76	2.7E-01	AF059043.1	EST_HUMAN	AV059043 ADB Homo sapiens cDNA clone ADBCD005.5'
8187	18082	28333	4.09	2.7E-01	AJ133269.1	NT	AV059043 ADB Homo sapiens cDNA clone ADBCD005.5'
8368	18334		1.27	2.7E-01	X85297.1	NT	Homo sapiens carotid-1/2 box, Contig1, D78522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
8910	19320		2.19	2.7E-01	AF217491.1	NT	G. gallus mRNA for tyrosine receptor type 3
462	12587	20224	1.54	2.9E-01	P78411	SWISSPROT	Homo sapiens fragile 160 nucleotide (FOR) gene, exon 6
472	10416		1.39	2.9E-01	P19439.1	NT	PROJ015-CLUST3 HOMEOBOX-DOMAIN PROTEIN RX-2
1371	11277	21133	2.23	2.9E-01	B598087.1	EST_HUMAN	Bos taurus mRNA for mb-1, complete cds
1418	11324	21188	0.97	2.9E-01	AB015360.1	NT	001010388F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE3972345 5'
1854	11760	21624	8.59	2.9E-01	AL161472.2	NT	Glycine max pseudogene for Bd 30K
1854	11760	21625	8.59	2.9E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
						NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
						EST_HUMAN	bio4010.1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE2996451 3' similar to gb:M35072.605
						EST_HUMAN	bio4010.1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE2996451 3' similar to gb:M35072.605
2046	11937		9.9	2.9E-01	AW733152.1	EST_HUMAN	REDSOMAL PROTEIN L7A (HUMAN); gb:M14689.cts1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2106	11995	21895	1.2	2.9E-01	MT1844.1	NT	Human prealbumin gene, complete cds
2424	12301		2.68	2.9E-01	Y12966.1	NT	B. maritimus fcd_ gene
2498	12374		9.98	2.9E-01	BE272440.1	EST_HUMAN	601120076F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE2900043 5'
3033	12960		1.03	2.9E-01	AW974531.1	EST_HUMAN	EST3385055 IMAGE2900043 5'
3485	13401		0.94	2.9E-01	BE217816.1	EST_HUMAN	h3b202.1 X1 NC1_CGAP_L104 Homo sapiens cDNA clone IMAGE3174914 3' similar to contains L1, L3, L1 repetitive element;
3532	13448	23245	1.12	2.9E-01	MT2342.1	NT	Bacteriophage T2 DNA (edman-N6)methyltransferase (dam) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3591	13505	23295	1.7	2.0E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3591	13505	23351	0.9	2.0E-01	AB017446.1	NT	Rattus norvegicus mRNA for organic anion transporter 3, complete cds
4010	13918	23891	1	2.0E-01	AF095970.1	EST HUMAN	Human alpha-actinin-1, complete cds
4002	13904	23742	13.13	2.0E-01	BC006598.1	EST HUMAN	QVT-BT0630-040000-132-003 BT0630 Homo sapiens cDNA
4259	14168	23935	0.95	2.0E-01	AF175293.1	NT	Enterococcus faecium strain N97/330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4393	14289	24072	0.84	2.0E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	14289	24073	0.84	2.0E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4448	14342	24134	1.17	2.0E-01	AA457617.1	EST HUMAN	ss89407.71 Stratiotes fetal retina 93/202 Homo sapiens cDNA clone IMAGE:339477.5
4548	14441	24224	1.83	2.0E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a-b-binding protein [Ltrca5.1] mRNA, complete cds
4816	14504	24292	1.26	2.0E-01	AF142703.1	NT	Ophiostoma redicola matricase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4993	14778	24554	3.53	2.0E-01	H04868.1	EST HUMAN	Y57A03.1 Soares fetal liver spliced INFLS Homo sapiens cDNA clone IMAGE:15238.5
5051	14823	24869	0.86	2.0E-01	PF05653	SWISSPROT	ACTYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MGAD)
5700	15764		2.03	2.0E-01	AE001811.1	NT	Thermotoga maritima section 123 of 138 of the complete genome
5793	15870	25777	1.93	2.0E-01	AI82357.1	EST HUMAN	502a12.4 NCL CGAP Panel Homo sapiens cDNA clone IMAGE:2227438.3 similar to SW:NDP1_RAT 304289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR; 1 repetitive element;
5793	15870	25778	1.93	2.0E-01	AI82357.1	EST HUMAN	502a12.4 NCL CGAP Panel Homo sapiens cDNA clone IMAGE:2227438.3 similar to SW:NDP1_RAT 304289 NEUROGENIC DIFFERENTIATION FACTOR 1, contains element LTR; 1 repetitive element;
6552	16410	26939	1.52	2.0E-01	R10365.1	EST HUMAN	Y57A03.1 Soares fetal liver spliced INFLS Homo sapiens cDNA clone IMAGE:15238.5
6565	16405	26956	1.27	2.0E-01	R02411.1	EST HUMAN	Y57A03.1 Soares fetal liver spliced INFLS Homo sapiens cDNA clone IMAGE:15238.5
6982	1673	29025	3.01	2.0E-01	BF343688.1	EST HUMAN	g01X287.01 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
6990	16779	26973	2.04	2.0E-01	Q10189	SWISSPROT	g01X287.01 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7048	16923	27112	4.34	2.0E-01	BE830339.1	EST HUMAN	HYPOPHYSICAL 75.2 RD PROTEIN CH1C1.02 IN CHROMOSOME II
7048	16923	27112	4.34	2.0E-01	BE830339.1	EST HUMAN	HYPOPHYSICAL 75.2 RD PROTEIN CH1C1.02 IN CHROMOSOME II
7048	16923	27113	4.34	2.0E-01	BE830339.1	EST HUMAN	HYPOPHYSICAL 75.2 RD PROTEIN CH1C1.02 IN CHROMOSOME II
7554	17704		1.16	2.0E-01	Q28395	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8812	18925		93.05	2.0E-01	X61755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9139	18902		1.96	2.0E-01	10190555	NT	Human lambda-immunoglobulin constant region complex (germline)
9328	19555		1.92	2.0E-01	BE838149.1	EST HUMAN	g01X1002F1 NIH MSC_71 Homo sapiens cDNA clone IMAGE:3512612.5
9395	19053	25309	2.6	2.0E-01	AF316996.1	NT	Homo sapiens NaHKAATase gamma subunit (PX7D2) gene, complete cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9653	19333		6.03	2.EE-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
9659	19376		1.5	2.EE-01	Q01031	SWISSPROT	ADENYLATE CYCLASE (ATP PYROPHOSPHATYLASE) (ADENYL CYCLASE)
241	10209	20025	2.12	2.EE-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
242	10209	20025	1.86	2.EE-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
255	10221		3.24	2.EE-01	M26501.1	NT	Starfish (<i>P. ochinotus</i>) cytoplasmic actin gene, complete cds
815	10743	20659	1.32	2.EE-01	U06904.1	NT	Mus musculus CRI/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-5) gene, complete cds
1044	10902		1.85	2.EE-01	AE002166.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1105	11021	20984	9.6	2.EE-01	T89837.1	EST HUMAN	yw1g07.f1 Stragelung lung (4537210) Homo sapiens cDNA clone IMAGE:117468 6'
1633	11407	21268	0.85	2.EE-01	AL115624.1	NT	Botrytis cinerea strain 14 cDNA library under conditions of nitrogen deprivation
1697	11509		5.43	2.EE-01	4895406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1840	12706	21012	0.83	2.EE-01	BE596904.1	EST HUMAN	PM4-CT040-310700-005-008 CT0400 Homo sapiens cDNA
1840	12706	21613	0.83	2.EE-01	BE596904.1	EST HUMAN	PM4-CT040-310700-005-008 CT0400 Homo sapiens cDNA
2267	12237		8.29	2.EE-01	AE0090675.1	NT	Aquifex coelicola section 7 of 109 of the complete genome
2448	12323		1.38	2.EE-01	AA351087.1	EST HUMAN	orf1a12.1 NGI CGAP G081 Homo sapiens cDNA clone IMAGE:584882 5'
2597	12450	22359	0.97	2.EE-01	X83310.1	NT	B. latus mRNA for D-aspartate oxidase
3368	13285		2.87	2.EE-01	AW073471.1	EST HUMAN	EST1365404 IMAGE receptor, MAGN Homo sapiens cDNA
3460	13405	23211	0.85	2.EE-01	AF233875.1	NT	Danio rerio peptides YY precursor gene, complete cds
3502	13419	23220	7.93	2.EE-01	AL191517.2	NT	Arabidopsis thaliana DNA chromosome 4 contig fragment No. 26
3774	13686	23486	1.16	2.EE-01	AI741483.1	EST HUMAN	yw1g07.ct1 Soares NSF_F8_3W_OT_PA_P1 Homo sapiens cDNA clone IMAGE:2954780 3'
3774	13686	23486	1.16	2.EE-01	AI741483.1	EST HUMAN	yw1g07.ct1 Soares NSF_F8_3W_OT_PA_P1 Homo sapiens cDNA clone IMAGE:2954780 3'
3877	13884		0.83	2.EE-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4222	14120		1.2	2.EE-01	Q03314	SWISSPROT	RHB PROTEIN
4514	14407	24193	0.69	2.EE-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naiip6) gene, complete cds, and Naiip3 gene, exons 2-9 and 11-16
4543	14531		1.14	2.EE-01	C27225	SWISSPROT	MO1-INHIBITING HORMONE PRECURSOR (MIF)
4549	14535	24324	3.78	2.EE-01	AF007768.1	NT	Chlorodinium funiforme dipeptide associated protein 2 (DAP2) mRNA, complete cds
4672	14558	24351	2.19	2.EE-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 75 of 99 of the complete chromosome
4698	14584		3.16	2.EE-01	AJ201113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gap portion of MURV-L (murine endogenous retrovirus) element
4726	14612	24309	0.79	2.EE-01	BE690785.1	EST HUMAN	60143748B1.NIH_MSC_72 Homo sapiens cDNA clone IMAGE:3922600 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4760	14635	24421	0.89	2.5E-01	AB011070.1	NT	Mus musculus gene for uncoupling protein 3, 6'-flanking region and partial 5'UTR
5169	16035	24602	0.89	2.5E-01	AW959183.1	EST HUMAN	h17909.Y1 NOL CGAP: GU1 Homo sapiens cDNA clone IMAGE:2698049 5' similar to contains TAR1.12
5169	16035	24603	0.89	2.5E-01	AW959183.1	EST HUMAN	TAR1 repetitive element
5204	16186	24602	11.02	2.5E-01	SR3390.1	NT	h17909.Y1 NOL CGAP: GU1 Homo sapiens cDNA clone IMAGE:2698049 5' similar to contains TAR1.12
6390	16229	24602	1.32	2.5E-01	AF134119.1	NT	TAR1 repetitive element
6500	16360	26532	3.73	2.5E-01	AL163262.2	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6593	16403	26955	2.90	2.5E-01	BF100400.1	EST HUMAN	Homo sapiens chromosome 21 segment HS21C082
6788	16967	26958	2.26	2.5E-01	BF33956.1	EST HUMAN	7057a03.1 Soares NSF F6_5W_0T_PA_P_51 Homo sapiens cDNA clone IMAGE:3523369 3'
7020	16967	27087	3.95	2.5E-01	U89551.2	EST HUMAN	001456239F1 NH1 M3C_06 Homo sapiens cDNA clone IMAGE:3902809 5'
7481	17351	27654	16.11	2.5E-01	U89551.2	NT	X8407.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:202501 5'
7481	17351	27655	16.11	2.5E-01	AF985164.1	NT	Homo sapiens matrix metalloproteinase MMP Rask-1 gene, promoter region
7523	17341	27647	2.04	2.5E-01	AF985164.1	NT	Homo sapiens matrix metalloproteinase MMP Rask-1 gene, promoter region
7523	17341	27648	2.04	2.5E-01	AF985164.1	NT	Hordium vulgare receptor-like kinase LRK10 gene, partial cds
7614	17664	27604	1.5	2.5E-01	AW581097.1	EST HUMAN	Hordium vulgare receptor-like kinase LRK10 gene, partial cds
8010	17860	28105	1.62	2.5E-01	AW162246.1	EST HUMAN	RC3-ST0185-100100-016-a07 ST0186 Homo sapiens cDNA
8011	17861	28105	1.68	2.5E-01	AW162246.1	EST HUMAN	sgf10.01 NOL CGAP: LH1 Homo sapiens cDNA clone IMAGE:2630094 3' similar to contains Alu repetitive element
8425	18300	28655	2.32	2.5E-01	D50741.1	NT	described combining element MSR1 repetitive element
9074	18891	29117	2.46	2.5E-01	AF205268.1	NT	Human mRNA for KIAA0124 gene, partial cds
9100	18729	28672	4.2	2.5E-01	AF161641.2	NT	Zea mays cellulose synthase-4 (Cesa4) mRNA, complete cds
9590	10891	26072	1.28	2.5E-01	AF170072.1	EST HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
9411	10482	20362	1.93	2.4E-01	AA939316.1	EST HUMAN	Spodoptera frugiperda CALNIN mRNA, complete cds
8301	10757	20908	2.38	2.4E-01	BF979124.1	EST HUMAN	001456239F1 NH1 M3C_06 Homo sapiens cDNA clone IMAGE:3523369 3'
1282	11190	21041	17.41	2.4E-01	AJ269880.1	NT	922132442F1 NH1 M3C_06 Homo sapiens cDNA clone IMAGE:1662023 3'
1282	11190	21042	17.41	2.4E-01	AJ269880.1	NT	922132442F1 NH1 M3C_06 Homo sapiens cDNA clone IMAGE:1662023 3'
1392	11298	21723	1.04	2.4E-01	Y17293.1	NT	Homo sapiens KIAA0851 gene (partial), X13 gene and LZ1F1 gene
1808	11705	21629	2.408	2.4E-01	AF267763.1	NT	Homo sapiens FL1 gene, partial
1855	11754	21629	1.41	2.4E-01	AF267763.1	NT	Measurmentum crystallinum putative potassium channel protein M1p1p mRNA, complete cds
2091	11990	21975	0.88	2.4E-01	AF111053.2	NT	Zoecia diaphanoides fructose-1,6-bisphosphatase mRNA, complete cds
2122	12010	21975	1.16	2.4E-01	AF111053.2	NT	Zoecia diaphanoides fructose-1,6-bisphosphatase mRNA, complete cds
2216	12101	22006	2.01	2.4E-01	AE000380.1	NT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAT PROTEASE)
2216	12101	22006	2.01	2.4E-01	AE000380.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HR BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2832	12213	22111	0.85	2.4E-01	BF002171.1	EST_HUMAN	7123d04.x1 NCL CGAP Cor16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:FRS8_XENLA
2491	12366	22260	1.63	2.4E-01	X73554.1	NT	O42890.203 PROTEASE REGULATORY SUBUNIT 6A ;
2734	12506	22491	2.14	2.4E-01	AJ71783.1	NT	D discoidium (A3-K) pona gene
2756	12818	22510	6.68	2.4E-01	AF030154.1	NT	S pombe sw6 gene
3093	13020		2.82	2.4E-01	U72726.1	NT	Bovine adenovirus 3 complete genome
3109	13035	22831	1.85	2.4E-01	X74206.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrof (gag/pol) genes, complete cds
4817	14700	24486	0.89	2.4E-01	BE106080.1	EST_HUMAN	H sapiens AGT gene, Pefl fragment of intron 4
4881	14856	24622	50.15	2.4E-01	D00944.1	NT	QV-HT0412-020400-135-510 HT0412 Homo sapiens cDNA
5480	15389	25451	7.53	2.4E-01	AF091216.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5480	15389	25452	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5593	15508	25553	2.13	2.4E-01	BF092336.1	EST_HUMAN	Mus musculus Wm protein (Wm) gene, complete cds
5642	15555	25648	2.69	2.4E-01	AF035546.1	NT	7154d04.x1 NCL CGAP B-118 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
5705	15813	25714	2.16	2.4E-01		NT	O08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element
5837	15842	25856	1.79	2.4E-01	AF065956.1	EST_HUMAN	Drosophila melanogaster p38a MAP kinase gene, complete cds
6543	15208	26371	3.87	2.4E-01	L43071.1	NT	Homo sapiens HSPG142 protein (HSPG142) mRNA
6590	16739	26931	1.62	2.4E-01	AJ075851.1	NT	hsc82-11.x1 NCL CGAP P-act1 Homo sapiens cDNA clone IMAGE:2322220 3' similar to gb:U08464
7617	17305	27511	6.72	2.4E-01	AF069515.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7665	17815	28050	1.93	2.4E-01	Q03992	SWISSPROT	Bov taurin guanyllyl cyclase-activating protein 2 (guad2) mRNA, complete cds
8149	18037	28285	3.83	2.4E-01	AF101494.2	NT	1 embryonal thymoplasma macrophage gene encoding ribosomal protein L3, events 1-2
8209	18093	28347	1.99	2.4E-01	AF030169.1	NT	wd4502.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contents
8534	18406		2.42	2.4E-01	Z21647.1	NT	ME222k1 TART repetitive element;
9030	18821	29109	1.55	2.4E-01	AF217491.1	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
9162	19526		2.39	2.4E-01	AF004218.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
9222	19345		2.54	2.4E-01	AJ276191.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
9439	19509		1.59	2.4E-01	V01507.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
9650	19716		1.26	2.4E-01	BF229975.1	EST_HUMAN	P. asiatica mosaic virus genomic RNA
9893	19355		3.33	2.4E-01	AF163281.2	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exon 6
383	10330	20153	0.8	2.8E-01	J75688.1	NT	Arabidopsis thaliana ethylene-insensitive-1 (EIL1) mRNA, complete cds
						NT	Mus musculus mRNA for putative mcr7 protein (mcr7 gene)
						NT	Gallus gallus gene coding for a-actin
						NT	RC3-CT0413-100800-022-506 CT0413 Homo sapiens cDNA
						NT	Homo sapiens chromosome 21 segment HS21C081
						NT	aromallase [Procellipha guttata-zabala finches, ovary, mRNA, 3189 nt]

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
621	10558		4.42	2.3E-01	U39713.1	NT	Myoplasma genitalium section 35 of 51 of the complete genome
651	10397	20403	19.84	2.3E-01	U07598.1	NT	Melanococcus janashii section 135 of 150 of the complete genome
918	10842	20697	3.35	2.3E-01	BE31189.1	EST_HUMAN	001142079T NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3005818 5'
1464	11368	21258	1.5	2.3E-01	6677690	NT	Mus musculus nucleolar protein sorting 48 (yeast) (Yps48), mRNA
1546	11451		0.89	2.3E-01	U22837.2	NT	Yersinia pseudotuberculosis Hmef1 (hmfE), Hmef2 (hmfF), Hmef3 (hmfG), and Hmef4 (hmfS) genes, complete cds
1589	11460	21351	1.39	2.3E-01	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
1914	11519	21376	2.75	2.3E-01	Y10397.2	NT	Mus musculus cdc15 gene, exon 1, partial
1998	11802		1.3	2.3E-01	AJ23535.1	NT	Homo sapiens partial intron 3 of the wild type A7-4/FEL gene
2368	12274	22160	1.56	2.3E-01	BE207718.1	EST_HUMAN	001175562T NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2915	12483	22372	1.02	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2764	11271	21127	0.89	2.3E-01	AB015033.1	NT	Maintenella spirochaetae cybB gene for DNA gyrase subunit B, partial cds, strain:FO 14507
2934	12861	22861	1.28	2.3E-01	AA601378.1	EST_HUMAN	not found x1 NGL CGAP Phel1 Homo sapiens cDNA clone IMAGE:1100943 3' similar to contains Alu
3045	12972		5.73	2.3E-01	R21723.1	EST_HUMAN	testis-specific element/containing element THR repetitive element
3324	13214	22051	1.03	2.3E-01	H03636.1	EST_HUMAN	0075101T Soares fetal liver species 1HLS Homo sapiens cDNA clone IMAGE:213283 5'
3766	13079	23451	1.11	2.3E-01	SC2921.1	NT	GS1A-5-glyceraldehyde 3-phosphate dehydrogenase 1 (c13)
3856	13767		3.72	2.3E-01	7602193	NT	Homo sapiens KIAA0450 gene product (KIA0450), mRNA
4293	14152	23029	0.85	2.3E-01	R02522.1	EST_HUMAN	01701.T1 Soares placenta N232P Homo sapiens cDNA clone IMAGE:149017 5'
4500	14166		3.35	2.3E-01	R78769.1	NT	Mus musculus trna (Phe-10) gene, promoter region
4546	14245	24031	1.02	2.3E-01	D00690.1	NT	Synchrystallin sp. PC-58003 complete genome, 1/27 1-133959
4596	14282	24051	2.05	2.3E-01	AF092351.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM-3), mRNA, complete cds
4454	14348	24140	5.1	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (nuclear protein 15) (NP15) mRNA
4996	14668	24455	0.82	2.3E-01	J03280.1	NT	Homo sapiens phenylethanolamine N-methyltransferase gene, complete cds
5002	14877	24641	0.95	2.3E-01	BF10135.1	EST_HUMAN	001809138T NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4123358 5'
5101	14669	24745	0.68	2.3E-01	L01328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (p-LA-H) gene, Racket gene, and sodium phosphate transporter (NP-73) gene, complete cds
5145	15013	24763	26.95	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5245	15169	24942	2.9	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5332	15252	25074	1.71	2.3E-01	BF058391.1	EST_HUMAN	74300606.x1 NCL CGAP OV18 Homo sapiens cDNA clone IMAGE:3476990 3' similar to SW-GAG_SNSAV P08330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P26; NUCLEOPROTEIN P10] ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6395	10314	25361	4.83	2.3E-01	X65987.1	NT	Citofilin (non) gene
6518	15533	25617	1.87	2.3E-01	A1709840.1	EST_HUMAN	sa2761241 Barbed sorta HFLRB6 Homo sapiens cDNA clone IMAGE:2818448 3' similar to gbX13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6518	15533	25618	1.87	2.3E-01	A1709840.1	EST_HUMAN	sa2761241 Barbed sorta HFLRB6 Homo sapiens cDNA clone IMAGE:2818448 3' similar to gbX13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6111	16025	28142	3.93	2.3E-01	A1718148.1	EST_HUMAN	sa4291212 Barbed sorta HFLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains ALU repetitive element;
6394	16246	29409	2.02	2.3E-01	AF171399.1	NT	Glycine max (resistance) protein LMI7 precursor RNA, partial cds
6487	16345	28519	3.19	2.3E-01	67647670	NT	Mus musculus (mouse X) (Mmu)15. mRNA
6491	16349	28519	1.89	2.3E-01	BE68071.1	EST_HUMAN	8016157565 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3012689 5'
6500	16418		2.9	2.3E-01	N09393.1	EST_HUMAN	sa25498.1 Soares fetal liver spiken N1VLS Homo sapiens cDNA clone IMAGE:262658 5'
6664	16544	28741	2.28	2.3E-01	M69851.1	NT	Oxyferritin non-metronuclear ferritin-binding protein alpha subunit (beta-alpha alanine version) gene, complete cds
7657	17507	27732	4.37	2.3E-01	X62124.1	NT	Haemophilus influenzae genes for H3N1 restriction-modification system (H3N1 methyltransferase (EC 3.1.1.72) and H3N1 endonuclease (EC 3.1.21.4))
7712	17562	27871	2.64	2.3E-01	BE173000.1	EST_HUMAN	RHO4110599-240400-014-g11 H10559 Homo sapiens cDNA
7740	17590	27871	2.26	2.3E-01	A1902681.1	NT	Plutonium-10959-240400-014-g11 H10559 Homo sapiens cDNA
7974	17824		4.95	2.3E-01	BF13577.1	EST_HUMAN	M140616592 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102062 3'
8525	18337	29603	2.84	2.3E-01	A1250189.1	NT	Mus musculus partial mRNA for muscle protein 934 (mg934 gene)
8525	18397	29654	2.84	2.3E-01	A1250189.1	NT	Mus musculus partial mRNA for muscle protein 934 (mg934 gene)
8698	18647	29830	2.39	2.3E-01	A1002167.2	EST_HUMAN	Chlamydomonas reinhardtii AR99, section 4 of 64 of the complete genome
9144	18868		2.93	2.3E-01	A16526.1	NT	Borealis bacteriophage 2.65 locus, ORF-4.0D genes, complete cds and REP+ gene, partial cds
9332	18951		20.48	2.3E-01	7727291.1	EST_HUMAN	HO0587141 HT22046 Homo sapiens cDNA clone IMAGE:4148
9238	19471		1.05	2.3E-01	A1008819.1	EST_HUMAN	chr1434.3eq.F Homo sapiens fetal blood, Lambda ZAP Express+ Homo sapiens cDNA 5'
9266	19570		2.07	2.3E-01	A17653940.1	EST_HUMAN	PMH-SN0012-030400-001-456 SN0012 Homo sapiens cDNA
9324	19665	24990	2.05	2.3E-01	AW303623.1	EST_HUMAN	sa251d07.41 Soares, N1V_L_GBC.S1 Homo sapiens cDNA clone IMAGE:2813775 3' similar to TR-Q82715 QB217411 Yseryl, OXNASE-RELATED PROTEIN 2, contains PRG.621 TART repetitive element;
9399	19708	24905	4.88	2.3E-01	BE682464.1	EST_HUMAN	8016072025 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3300889 5'
9407	19708		1.93	2.3E-01	BF693319.1	EST_HUMAN	8021444692 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4287719 5'
9495	19899		2.09	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9549	19939		4.54	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9703	19310		2.97	2.3E-01	BF475911.1	EST_HUMAN	nc838121.1 Lopek, sciatic nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element MEM38 (negative element);

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
84	10098	19885	0.90	2.2E-01	AF021600.1	EST_HUMAN	act4a10.1l Scores, fetal_liver, spleen, _INFLS_S1 Homo sapiens cDNA clone IMAGE:197920 3' similar to TRQ10040 Q10040 ATP-BINDING CASSETTE PROTEIN;
1945	11450	21311	3.13	2.2E-01	AF187890.1	NT	Homo sapiens PPAR delta gene, promoter region
1972	11885	-	0.91	2.2E-01	AF174001.1	NT	Timecourse malate dehydrogenase cytochrome c gene, partial cds; mitochondrial gene for mitochondrial product
2042	11983	21829	2.78	2.2E-01	AF04400.1	NT	Fresh-water sponge Emfil alpha collagen (COLF1) gene
2354	12234	22131	0.24	2.2E-01	BF07538.1	EST_HUMAN	602085058F1 NIH LMGC 83 Homo sapiens cDNA clone IMAGE:426989 5'
2543	12417	22307	2.41	2.2E-01	BE016298.1	EST_HUMAN	801463258F1 NIH LMGC 67 Homo sapiens cDNA clone IMAGE:3965180 5'
2543	12417	22305	2.41	2.2E-01	BE016298.1	EST_HUMAN	801463258F1 NIH LMGC 67 Homo sapiens cDNA clone IMAGE:3965180 5'
2563	12781	22570	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-H10353-281728-003-003-012 HT0353 Homo sapiens cDNA
2563	12781	22571	4.04	2.2E-01	BE155625.1	EST_HUMAN	PM2-H10353-281728-003-012 HT0353 Homo sapiens cDNA
2590	12817	-	1.59	2.2E-01	AF020503.1	NT	Homo sapiens FRAXB common fragile region, diadenosine triphosphate hydrolase (FHL1) gene, exon 5
3348	13286	-	2.67	2.2E-01	AL015692.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3743	13655	-	1.05	2.2E-01	AF155728.1	NT	Xenopus laevis nucleolar protein 1, nucleolar protein 1 (Nucleolar protein 1) pseudogene
4007	13913	22688	0.81	2.2E-01	AF113391.1	NT	Mus musculus ATP-binding cassette protein (Abc5) mRNA, partial cds
4118	14018	-	1.10	2.2E-01	AF110102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4125	14025	22800	5.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (MLK3) and two pore domain K+ channel subunit (Kcnk8) genes, complete cds
4165	14058	22840	1.97	2.2E-01	AF117360.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4165	14068	22841	1.97	2.2E-01	AF117360.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4258	14157	22633	1.16	2.2E-01	U07307.1	NT	Human scRNA (BC200 beta) pseudogene
4258	14157	22634	1.16	2.2E-01	U07307.1	NT	Human scRNA (BC200 beta) pseudogene
4305	14294	24078	1.09	2.2E-01	Z54148.1	NT	B. acutus hp28 gene
4719	14605	-	1.22	2.2E-01	D50504.1	NT	Human beta-cytoplasmic actin (ACTB) pseudogene
4724	14810	24388	2.47	2.2E-01	AA011216.1	EST_HUMAN	af070501.1 Stralagen (NT neuron (6637233) Homo sapiens cDNA clone IMAGE:94888 5'
4801	14771	24549	1.19	2.2E-01	MB0524.1	NT	Human cytochrome gene
4875	14950	-	1.2	2.2E-01	U13299.1	NT	Mus musculus myosin gene, exon 3
5913	15431	25495	1.71	2.2E-01	6903002	NT	Mus musculus diaphanous (Drosophila, homologue 2 (DIAPH2), transcript variant 195, mRNA
5918	15438	-	3.99	2.2E-01	D64000.1	NT	Synuclein-like protein, PC060603 complete genome, 1927, 2392729-2392869
6169	16074	26223	10.59	2.2E-01	AF175228.1	EST_HUMAN	AV175228 BM Homo sapiens cDNA clone IMAGE:3965180 5'
6319	16182	26342	2.01	2.2E-01	M24136.1	NT	Human glycoprotein B gene, exon 4
6319	16182	26343	2.01	2.2E-01	M24136.1	NT	Human glycoprotein B gene, exon 4
6676	16556	-	2.19	2.2E-01	AF155143.1	NT	Mus musculus rrm23-M1 gene, promoter region
7157	17034	27227	4.27	2.2E-01	AF001713.1	NT	Thermococcus maritima section 25 of 136 of the complete genome

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Describer
7217	17094		2.28	2.2E-01	AW95069.1	EST_HUMAN	P18-C10283-24198-008-007 C10283 Homo sapiens cDNA
7270	17147	27341	1.66	2.2E-01	6393247	NT	Mus musculus deformed epidermal autolytic factor 1 (Droscophila) (Dcaf1), mRNA
7304	17180	27382	1.39	2.2E-01	BF370334.1	EST_HUMAN	Mus musculus deformed epidermal autolytic factor 1 (Droscophila) (Dcaf1), mRNA
7353	17221	27421	1.4	2.2E-01	W02988.1	EST_HUMAN	Mus musculus deformed epidermal autolytic factor 1 (Droscophila) (Dcaf1), mRNA
7366	17344	27550	13.13	2.2E-01	P48954	SWISSPROT	LARGE PROLINE-RICH PROTEIN BA72 (LARP-ASSOCIATED TRANSCRIPT 2)
7397	17315	27522	3.96	2.2E-01	MB9643.1	NT	Brachydanio rerio epandrin beta and gamma chains (Epc) gene, complete cds
7648	17498	27720	3.57	2.2E-01	AF187941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CP-HSP21) mRNA, complete cds; nuclear gene for chloroplast product
7719	17599	27794	2.2	2.2E-01	BF206507.1	EST_HUMAN	80196972AF1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
8729	18540	28824	4.94	2.2E-01	X01918.1	NT	Drosophila 68K glue gene cluster
8766	17005	28140	2.91	2.2E-01	7706216	NT	Homo sapiens H-2K binding factor-2 (LOC571583), mRNA
6077	18954		2.2	2.2E-01	BE870669.1	EST_HUMAN	801446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:386970 5'
9183	18720		3.72	2.2E-01	U2871.2	NT	Homo sapiens chromosome Xc28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAC (PH dehydrogenase-like protein (NSDHL), and Lp
8269	18978		2.34	2.2E-01	AF189943.1	EST_HUMAN	Vitis rotundifolia cv1199-212-304 C10249 Homo sapiens cDNA
9379	15093	24687	2.65	2.2E-01	AF351098.1	EST_HUMAN	RC1-C10248-141199-212-304 C10249 Homo sapiens cDNA clone GKCA1802 5'
9875	18713		3.75	2.2E-01	AF592801.1	EST_HUMAN	hms1011.1 NGL CGAP Lip2 Homo sapiens cDNA clone IMAGE:1061804
955	10870	20727	1.74	2.1E-01	AA592869.1	EST_HUMAN	Archaeops halima DNA chromosome 4 contig fragment No. 16
958	10881	20729	0.9	2.1E-01	AL161504.2	NT	Chlamydomonas reinhardtii, section 45 of 53 of the complete genome
1108	11023		2.16	2.1E-01	AB023142.2	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1150	11091	20699	1.24	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1180	11091	20637	1.24	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1871	11797	21042	1.84	2.1E-01	AA000824.1	EST_HUMAN	dk7602.51 NGL CGAP G04 Homo sapiens cDNA clone IMAGE:1619610 3' similar to gb:K02765
2111	12000	21899	3.08	2.1E-01	BF660073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
							802085128F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247903 5'
2884	12821	22013	1.65	2.1E-01	0912445	NT	Homo sapiens potassium voltage-gated channel, subfamily H1 (seg-related), member 4 (KCNH4), mRNA
3756	13948		5.05	2.1E-01	8693061	NT	Beta vulgaris mitochondrion, complete genome
3957	13974	22651	1.01	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE190
3907	13974	22652	1.01	2.1E-01	P11075	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE190
4279	14178		1.28	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1216 protein, partial cds
4474	14368	24167	1.21	2.1E-01	AB010273.1	NT	Homo sapiens p18cat47 gene, complete cds
4766	14951	24439	1.26	2.1E-01	AA009784.1	NT	Homo sapiens hox11 prob- oncogene, exons 1 to 3 and 1ug-1 gene

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HNT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5134	15001	24772	0.69	2.1E-01	M82691.1	NT	Saccharomyces cerevisiae <i>tsi1</i> (TSC) gene, complete cds
5243	15070	24938	5.59	2.1E-01	BF672665.1	EST_HUMAN	R92152001 (F1) NH ₂ M3C 81 Homo sapiens cDNA clone IMAGE:4239001 F
6123	15167	29106	1.89	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
6385	16247	29106	1.67	2.1E-01	AF030072.1	NT	<i>Archaeoglobus fulgidus</i> section 135 of 172 of the complete genome
6535	16393	26572	1.74	2.1E-01	AF030049.1	NT	<i>Canis familiaris</i> <i>keratin</i> (KRT9) gene, complete cds
6559	16417	26596	1.35	2.1E-01	AF068937.1	NT	Glycine max <i>malate dehydrogenase</i> (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6559	16417	26597	1.35	2.1E-01	AF068937.1	NT	Glycine max <i>malate dehydrogenase</i> (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6705	16595		1.21	2.1E-01	7305630	NT	<i>Mus musculus</i> <i>cytochrome P-450</i> 3A11 (CYP3A11) gene, exon 8, 9, and partial cds
6951	18629	27022	4.78	2.1E-01	U63393.1	NT	<i>Haemophilus influenzae</i> <i>hmdC</i> , putative haemoglobin processing protein (hmdC), and haemoglobin immunity protein (hmdC) genes, complete cds
7224	17101	27289	5.85	2.1E-01	Z58758.1	NT	<i>Saccharomyces cerevisiae</i> <i>tsi1</i> (TSC) gene, complete cds
7479	17349	27553	2.35	2.1E-01	X97378.1	NT	<i>A. thaliana</i> <i>miR156</i> for <i>AtWRKY10</i> protein
7647	17388	27611	1.19	2.1E-01	AB036659.1	NT	Homo sapiens <i>p352</i> gene for ribonucleotide reductase, exon 8
7677	17787	28008	2.48	2.1E-01	Z67067.1	NT	<i>Salix viminalis</i> <i>miR156</i> for <i>AtWRKY10</i> protein
7629	17779	28018	1.49	2.1E-01	F62824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
8849	18691		2.31	2.1E-01	1109647	NT	(80 KD) DIACYLGLYCEROL KINASE
8902	18874	28954	2.15	2.1E-01	BE18422.1	EST_HUMAN	Homo sapiens pancreatic polypeptide 2 (PP2Y), mRNA
9622	19132		1.9	2.1E-01	AF217490.1	NT	R33-H10622 0.0600-013-011 H10622 Homo sapiens cDNA
9730	19634		1.4	2.1E-01	L32598.1	NT	Homo sapiens <i>fragile 100</i> oddo reductase (FOR) gene, exon 8, 9, and partial cds
9805	19382	25174	1.29	2.1E-01	BE672330.1	EST_HUMAN	Human <i>grainin</i> gene
9979	19439		1.29	2.1E-01	8835804	NT	<i>Salix viminalis</i> <i>miR156</i> for <i>AtWRKY10</i> protein
103	10165	10983	1.72	2.0E-01	AB017497.1	NT	<i>Salix glauca</i> <i>miR156</i> for <i>AtWRKY10</i> protein
523	10495		2.39	2.0E-01	7705601	NT	Homo sapiens <i>CSH-18</i> protein (LOC-51009), mRNA
684	10617	20440	1.19	2.0E-01	MT7085.1	NT	O. carolinensis <i>germin</i> light heavy chain V-H pseudogene, allele V-H2
793	10722	20593	1.81	2.0E-01	AF027865.1	NT	<i>Mus musculus</i> <i>Major Histocompatibility Locus</i> class II region
995	10915	20759	1.03	2.0E-01	D00905.1	NT	<i>Synchocystis</i> sp. PCC-8803 complete genome, 7127, 781449-920915
1109	11024	20896	2.67	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1234	11411	20963	1.42	2.0E-01	AJ132065.5	NT	Homo sapiens <i>ret</i> gene
1286	11104	21047	1.29	2.0E-01	AW34637.1	EST_HUMAN	PM1-H10422-292/292-002-006 H10422 Homo sapiens cDNA
1471	11376	21241	13.51	2.0E-01	4933408	NT	Homo sapiens <i>dystrobrevin</i> , alpha (DTNA), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1534	11438	21295	2.51	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0806
1938	11442	21300	1.59	2.0E-01	AF290700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1088	11950	21301	1.82	2.0E-01	AF111703.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1723	11824	21302	1.64	2.0E-01	U07625.1	NT	Methanococcus jannaschii section 67 of 160 of the complete genome
1847	11743	21618	1.33	2.0E-01	BE871330.1	EST HUMAN	001449441FT NIH_M3C_65 Homo sapiens cDNA IMAGE3853330 5'
1847	11743	21619	1.33	2.0E-01	BE871330.1	EST HUMAN	001449441FT NIH_M3C_65 Homo sapiens cDNA IMAGE3853330 5'
2299	12181	21619	1.57	2.0E-01	X82877.1	NT	H sapiens Na ⁺ -D-glucose cotransport regulator gene
2881	12789		0.95	2.0E-01	AF074690.1	NT	Homo sapiens full length insert cDNA YH5411
3442	13359	23166	0.8	2.0E-01	P46907	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HO-ZIP PROTEIN ATHB-10)
3520	13436		0.89	2.0E-01	AW280905.1	EST HUMAN	xp15602.x1 NCI CGAP_HN6 Homo sapiens cDNA clone IMAGE2740395 3' similar to contains element
3949	13560	23349	0.81	2.0E-01	P34481	SWISSPROT	MEP21 repetitive element ;
3945	13853	23626	0.8	2.0E-01	X83997.1	NT	CED-11 PROTEIN
4484	14358		8.47	2.0E-01	BE829165.1	EST HUMAN	G parasitica espC gene
4589	14729	24519	1.07	2.0E-01	AF147083.1	NT	OYA-EN0035:16900-223-403 EN0032 Homo sapiens cDNA
4972	14847	24618	8.07	2.0E-01	Y19216.1	NT	Homo sapiens gamma-glutamyl bicyclic gene, exon 8 and 9 and complete cds
5041	14913	24687	1.11	2.0E-01	X95900.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase for cell fusion, exon 1 to 9
5342	15263	25089	2.55	2.0E-01	X95900.1	NT	Homo sapiens putative pathBD pseudogene for cell fusion, exon 1 to 9
5510	15428	25497	2.13	2.0E-01	U16300.1	NT	Rat SOD2 gene for manganese-containing superoxide dismutase
5594	15603	25705	5.28	2.0E-01	U16300.1	NT	Homo sapiens dual oxidase-like domain 2 (DUOX2) mRNA
5574	15780	25800	4.31	2.0E-01	X61033.1	NT	Saccharomyces cerevisiae Hsp90 (Hsp90) mRNA, complete cds
5694	15839	25862	3.54	2.0E-01	AF360885.1	EST HUMAN	Maarutia mur class glutathione transferase gene
6937	19517		0.95	2.0E-01	AF028028.1	NT	PM1-CT0297:141099-001-g06 C10247 Homo sapiens cDNA
6772	19551	26839	4.18	2.0E-01	X91151.1	NT	Andes virus strain C123193 glycoprotein G1 and G2 precursor, gene, partial cds
7511	17299		4.39	2.0E-01	AF001278.1	NT	M. musculus sep2 gene exon 14
7692	17542		2.07	2.0E-01	AF145992.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
7774	17624	27857	1.95	2.0E-01	AF098907.1	NT	Homo sapiens titamin 2 (TLN2) mRNA, complete cds
7774	17624	27858	1.95	2.0E-01	AF098907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18058	28350	2.7	2.0E-01	AF098908.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18058	28351	2.7	2.0E-01	AF098908.1	NT	Salvelinus plusvius mRNA for transferrin, complete cds
9303	19119		1.37	2.0E-01	AF200637.2	NT	Pimphales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
9747	19308	25202	3.22	2.0E-01	A022592.1	EST HUMAN	ovb10.0.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE: 643610 3'
9769	19368		6.61	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9897	18374	25183	1.5	2.0E-01	11528465	NT	Mus musculus fructose 3 kinase (F3kl), mRNA
105	10088		10.35	1.9E-01	7549743	NT	Rattus norvegicus Ary hydrocarbon receptor nuclear translocator 1 (Ahnr), mRNA
349	10368	20126	8	1.9E-01	AF004383.1	NT	Mus musculus pde (ar) gene, wild type allele, 3' region, partial cds
840	10577	20362	1.31	1.9E-01	U92681.2	NT	Human sapiens lamellipodia protein kinase C-interacting protein mRNA, complete cds
840	10577	20363	1.31	1.9E-01	U92681.2	NT	Human sapiens lamellipodia protein kinase C-interacting protein mRNA, complete cds
647	10584	20400	5.37	1.9E-01	BC507891.1	EST_HUMAN	RC3-BT0502:251159-011-301 BT0502 Homo sapiens cDNA
648	10584	20400	7.32	1.9E-01	BC507891.1	EST_HUMAN	RC3-BT0502:251159-011-301 BT0502 Homo sapiens cDNA
970	10683		1.61	1.9E-01	7505180	NT	Mus musculus interleukin 2 receptor, gamma chain (IL2rg), mRNA
1088	11004	20845	9.3	1.9E-01	AA358813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' and 3'
1348	11254	21110	2.3	1.9E-01	AF091282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1416	11322		3.91	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rpb-2) gene, complete cds
2330	12211	22109	3.31	1.9E-01	AF184623.1	NT	Human sapiens hypochloral protein FLJ10581 (FLJ10581), mRNA
2682	12619	22611	3.91	1.9E-01	J09006.1	NT	Symodon hispidus p53 gene, partial cds
2948	12834		5.55	1.9E-01	J09006.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3349	13369	23072	3.4	1.9E-01	D13107.1	NT	Mus musculus for immunoglobulin diversity region D1
3434	13351	23155	4.83	1.9E-01	R16487.1	EST_HUMAN	(42910.1) Scars fetal liver clones (NRS) Homo sapiens cDNA clone IMAGE-125547 5'
3735	13577	23432	0.95	1.9E-01	AF264017.1	NT	Rattus norvegicus polyomavirus deoxyribose gene, complete cds
3762	13675	23457	0.95	1.9E-01	AF264017.1	SWISSPROT	PAIR-RULE PROTEIN ODD-PAIRED
3910	13820	23500	3.02	1.9E-01	AF030784.1	EST_HUMAN	Schistosoma cercariae parasite DNA for cytoplasmic dynein heavy chain, complete cds
3982	13869	23576	1.89	1.9E-01	AF1754106.1	EST_HUMAN	GM3-CT0315-271169-045-911 CT0315 Homo sapiens cDNA
4138	14038	23813	1.05	1.9E-01	BC583493.1	EST_HUMAN	MRT-FN0010:260700-007-004 FN0010 Homo sapiens cDNA
4369	14255	24049	0.89	1.9E-01	AL161483.2	NT	Anopheles thalassini DNA chromosome 4, contig fragment No. 5
4682	14548	24335	0.84	1.9E-01	AF164380.1	EST_HUMAN	Puget rubripes genes encoding carboxyl phosphate synthetase II, myosin light chain, MAP2
4912	14791	24568	0.86	1.9E-01	AF164380.1	EST_HUMAN	L3-CT0215:180200-087-002 CT0215 Homo sapiens cDNA
4943	14821		1.04	1.9E-01	AF223642.1	NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
4982	14837	24605	1.11	1.9E-01	OC5239	SWISSPROT	KINESIN-LIKE PROTEIN KIF4
5031	14903	24675	1.03	1.9E-01	AJ251176.1	NT	Phoca vitulina partial avr2b gene for alpha adrenergic receptor 2B
5113	14861	24795	0.99	1.9E-01	AJ251176.1	NT	Phoca vitulina partial avr2b gene for alpha adrenergic receptor 2B
5123	14891		1.19	1.9E-01	AK831198.1	EST_HUMAN	h3g912x1 NCL CGAP_3036 Homo sapiens cDNA clone IMAGE-2238886 3' similar to gb:M21574 ALPHA
5153	15020	24793	0.99	1.9E-01	AF176055	EST_HUMAN	PIATELET DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);
5441	15391		4.28	1.9E-01	AF176055	EST_HUMAN	Mus musculus Notch gene homolog 3, (Drosophila) (Notch), mRNA
5453	15391		4.28	1.9E-01	AF176055	EST_HUMAN	Mus musculus Notch gene homolog 3, (Drosophila) (Notch), mRNA
5453	15391		4.28	1.9E-01	AF176055	EST_HUMAN	ACD RECEPTOR ALPHA-1 (HUMAN);
5466	15396	25446	7.67	1.9E-01	AF176055	EST_HUMAN	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
5598	15503		2.26	1.9E-01	AF133116.1	EST_HUMAN	AU133116.1 NT2P40 Homo sapiens cDNA clone IMAGE:31063 3' similar to contains MER13 repetitive element
6162	15119	24983	1.7	1.9E-01	R43212.1	EST_HUMAN	yy04a12.81 Soares infant brain 1NB Homo sapiens cDNA clone IMAGE:31063 3' similar to contains MER13 repetitive element
9423	16284	26446	1.43	1.9E-01	U09022.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
9449	16310	26476	3.06	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
9553	16538	26735	1.62	1.9E-01	AF161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
7041	16918	27109	12.89	1.9E-01	AE033024.1	NT	Homo sapiens mRNA for KIAA1188 protein, partial cds
9036	17630	28176	2.19	1.9E-01	AF161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
9038	17630	28177	2.19	1.9E-01	AF161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
8137	18025	28271	1.75	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
8991	18768	29020	2.61	1.9E-01	AJ243213.1	NT	Homo sapiens partial 6-H14 receptor gene, exons 2 to 5
9546	19146	19760	1.67	1.9E-01	AF059100.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
9830	19548		1.26	1.9E-01	AF001183.1	NT	Arabidopsis thaliana receptor-like kinase LEOR1 (LEOR1) gene, complete cds
26	10016	16811	2.26	1.9E-01	U76200.1	NT	Mus musculus p115Rb mRNA, complete cds
290	12683	22041	1.22	1.9E-01	AE022080.1	NT	Mus musculus Crag gene for chaperonin containing TGF- β gamma subunit, partial cds
866	10322	20146	2.41	1.9E-01	480262	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
929	10681	20463	2.16	1.9E-01	AB021490.2	NT	Cyprid, lilioid genes for morphine gumyl cyclase GGC1, complete cds
906	10689	20735	0.85	1.9E-01	AF072721.1	EST_HUMAN	wf1702.X1 NC CGAP U024 Homo sapiens cDNA clone IMAGE:2337651 3'
1075	10680	20852	1.21	1.9E-01	AF005960.1	NT	Drosophila discoidium plasmid DAP5, complete genome
1267	11174	21024	5.28	1.9E-01	AL117199.1	NT	Yersinia pestis plasmid pCD1
1487	11392	21252	1.29	1.9E-01	6763947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1487	11392	21253	1.29	1.9E-01	6763947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1803	11700		0.92	1.9E-01	486006	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1823	11720		1.92	1.9E-01	AF13708.1	EST_HUMAN	gg22010.x6 NC CGAP X43 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:075936 075936 GAMMA BUTYROBETAIN HYDROXYLASE
1873	11789	21644	1.6	1.9E-01	AB051897.1	NT	Mus musculus Soy6, Soy6e-pa, Soy6e genes for small inducible cyclin A8 precursor, small inducible cyclin A8 precursor, Soy6e pseudogene, small inducible cyclin A8 precursor, complete cds
2690	12527		2.99	1.9E-01	AF195728.1	EST_HUMAN	Q93-070018-081259-036-g04 D70018 Homo sapiens cDNA
2848	12795		1.61	1.9E-01	AF184389.1	NT	Jomquidium aculea LEAFY protein (LEAFY2) gene, partial cds
2873	12800	22595	1.09	1.9E-01	AF182300.1	EST_HUMAN	yH1403.X1 Soares, NF1_T_GBC S1 Homo sapiens cDNA clone IMAGE:2859756 3'
3085	13012	22803	1.28	1.9E-01	AF195578.1	EST_HUMAN	QV0-BN0041-070300-147-g04 BN0041 Homo sapiens cDNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	13494	23275	1.07	1.9E-01	H03399.1	EST_HUMAN	y4501.1a1 Soares placenta Nb21P Homo sapiens cDNA clone IMAGE:151704.3 similar to contains Alu repetitive element
3570	13494	23276	1.07	1.9E-01	H03399.1	EST_HUMAN	y4501.1a1 Soares placenta Nb21P Homo sapiens cDNA clone IMAGE:151704.3 similar to contains Alu repetitive element
4154	14054	23826	0.8	1.9E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
4238	14137	23765	1.13	1.9E-01	DG7654.1	NT	Bovine NB29 mRNA for MHC class II (B2J-DCB), complete cds
4486	14350	24141	5.12	1.9E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 95
4663	14549	24339	2.39	1.9E-01	AB051897.1	NT	Mus musculus Soy6b, Soy6b, Soy6b genes for small inducible cyclin A6 precursor, small inducible cyclin A9 precursor, Soy6b pseudogene, small inducible cyclin A5 precursor, complete cds
4700	14698	24377	0.93	1.9E-01	X02179.1	NT	S. uberozum mRNA for alcohol dehydrogenase
4977	14862	24618	1.77	1.9E-01	AF018420.1	EST_HUMAN	MF3-37038-151295-112-298 S10203 Homo sapiens cDNA
5027	14900	24670	4.17	1.9E-01	AF018428.1	NT	Mesocricetus auratus Nucleoside cotranscripting poly(ADP-ribose) mRNA, partial cds
5033	14938	24697	1.29	1.9E-01	AL43896.1	EST_HUMAN	1576d4.21 NC1 CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134562.3'
5177	14938	24697	1.03	1.9E-01	AJ007042.1	NT	Homo Sapiens hsp11 gene, 5' UTR
5346	15495	25535	1.41	1.9E-01	AL191594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5822	15527	25652	1.29	1.9E-01	CG01714	SWISSPROT	FORHEAD BOX PROTEIN E3
5943	15553	25652	2.25	1.9E-01	U04653.1	EST_HUMAN	y92102.71 Soares multiple actarous, 2NHLHSP Homo sapiens cDNA clone IMAGE:275163.5'
6176	16065	26214	1.38	1.9E-01	AB016591.1	NT	Citellus laurus mRNA for vaxs, complete cds
6176	16065	26215	1.38	1.9E-01	AB016591.1	NT	Citellus laurus mRNA for vaxs, complete cds
7382	17251	27458	1.22	1.9E-01	M73558.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
7386	17314	27521	1.22	1.9E-01	0628232	NT	Bacteriophage lta, complete genome
7633	17793	28022	1.19	1.9E-01	X03440.1	NT	M. musculus mRNA for P16-protein tyrosine phosphatase
8033	17925	28172	3.19	1.9E-01	X07336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
8086	17968	28206	6.95	1.9E-01	U08006.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, hsdR and lysis genes, complete cds
8118	19005	28214	2.9	1.9E-01	AB016591.1	NT	Citellus laurus mRNA for vaxs, complete cds
8118	19005	28215	2.9	1.9E-01	AB016591.1	NT	Citellus laurus mRNA for vaxs, complete cds
8119	19007	28264	3.88	1.9E-01	AF019107.1	NT	Dichytolium discoloratum unknown (DG10341) genes, complete cds
8391	19258	28507	2.64	1.9E-01	M56257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
8759	17607	29152	3.89	1.9E-01	X07303.1	NT	B. laurus mRNA for potassium channel
8976	19791	29073	2.83	1.9E-01	8394421	NT	Rattus norvegicus Thrombospondin receptor (Tbx22), mRNA
9169	18912	29344	1.65	1.9E-01	SP343923.1	EST_HUMAN	020201862951 NC1 CGAP Bmp67 Homo sapiens cDNA clone IMAGE:4155319.5'
9205	19200		2.05	1.9E-01	Q06962	SWISSPROT	CTA TERMINAL PROTEIN (BELLETTI PROTEIN) (PTP PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	19272		7.94	1.8E-01	R2484.1	EST HUMAN	JM4H10.1 Sources placenta N20HP Homo sapiens cDNA clone IMAGE:33027 5'
9779	19284		1.83	1.8E-01	JY1114.1	NT	E. dispar mRNA for hexokinase (hdxk)
863	10503	20309	1.8	1.7E-01	BE385164.1	EST HUMAN	60127406AF NIH LMGC_20 Homo sapiens cDNA clone IMAGE:3916788 5'
788	10717	20559	2.04	1.7E-01	X53330.1	NT	P. juliflor histone gene cluster for core histones H2A, H2B, H3 and H4
945	10870		1.89	1.7E-01	P38519	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
1042	10960	20802	1.6	1.7E-01	AF081810.1	NT	Lysenin disar nucleodiphenololactone, complete genome
1042	10960	20803	1.6	1.7E-01	AF081810.1	NT	Lysenin disar nucleodiphenololactone, complete genome
1838	11833		3.8	1.7E-01	AF255051.1	NT	Homo sapiens BNP3H (BNP3H) gene, complete cds; nuclear gene for mitochondrial product
2628	12756	22546	1.93	1.7E-01	AF000716.1	NT	Vitis chlorella hypoxanthine phosphoribosyltransferase (hpf) gene, partial cds, hemagglutinin/protease regulatory protein (hspR) gene, complete cds, and YRAL_VISCO gene, partial cds
2828	12758	22549	1.93	1.7E-01	AF000716.1	NT	Vitis chlorella hypoxanthine phosphoribosyltransferase (hpf) gene, partial cds, hemagglutinin/protease regulatory protein (hspR) gene, complete cds, and YRAL_VISCO gene, partial cds
2893	12823	22616	1.74	1.7E-01	AJ335509.1	EST HUMAN	EST J1565 Endometrial tumor Homo sapiens cDNA 5' and
2507	12894	22653	1.36	1.7E-01	AJ287336.1	NT	Naja nigra atr cdx-1 gene, exon 1-3
2507	12894	22654	1.35	1.7E-01	AJ287335.1	NT	Naja nigra atr cdx-1 gene, exon 1-3
3057	12994	22785	1.88	1.7E-01	AF081514.1	NT	Tactus candidatus geranylgeryanyl diphosphate synthase mRNA, complete cds
3401	13316	23119	1.99	1.7E-01	AJ265595.1	NT	Anabaena sp. ORF4 (paraf), ORF3, ORF2, ORF1, adpA gene, adpC gene, adpD gene, adpE gene and adpF gene
3557	13471	23262	1	1.7E-01	AJ224877.1	NT	Homo sapiens hsp1 gene, complete CDS
3559	13770	23692	4.41	1.7E-01	AJ238377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 9 of the AF-1/PEL gene
4459	14353		1.86	1.7E-01	X52959.1	NT	Salicicoccia grisea alpha repetitive DNA
4732	14617	24403	1.4	1.7E-01	AI247636.1	EST HUMAN	q157609.1 Sources, fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:1848693 3' similar to cortislin ORF.b1 ORF repetitive element
4966	14891		1.16	1.7E-01	U28376.1	NT	Xenopus laevis calcium-dependent protein kinase (M205P2) mRNA, complete cds
5097	14937		1.18	1.7E-01	AF072725.1	NT	Xenopus laevis branching enzyme IIIb (se) gene, complete cds
5321	15241	25046	1.76	1.7E-01	AA470986.1	EST HUMAN	nef3a2.21 NGL CGAP_C03 Homo sapiens cDNA clone IMAGE:881065 3' similar to gbM17895 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN)
5321	15241	25047	1.76	1.7E-01	AA470986.1	EST HUMAN	nef3a2.21 NGL CGAP_C03 Homo sapiens cDNA clone IMAGE:881065 3' similar to gbM17895 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN)
5820	15726	25839	12.31	1.7E-01	H71218.1	EST HUMAN	ye02608.31 Sources fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:273565 3'
6112	16006		2.16	1.7E-01	AF028552.3	NT	Miscicollaria aurata ovalactin precursor (OVI) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6320	16183	26344	7.99	1.7E-01	9C34179.1	EST_HUMAN	60706022F1 NH1.MGC.21 Homo sapiens cDNA clone IMAGE:3843984 5'
6938	16468	26988	1.2	1.7E-01	AF000573.1	NT	Homo sapiens homogenin-like 1, 2-deoxyglucose gene, complete cds
6914	16963	26982	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 79kD subunit (CPSF3), mRNA
6914	16963	26983	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 79kD subunit (CPSF3), mRNA
7086	16943	27135	2.46	1.7E-01	U00384.1	NT	Rat (SHR strain) Sx1 gene
7551	17352	27563	7.38	1.7E-01	AP001608.1	NT	Bacillus halodurans genomic DNA, section 2714
7601	17452	27666	2.06	1.7E-01	J16238.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7875	17725		2.42	1.7E-01	AL15284.2	NT	Homo sapiens chromosome 21 segment HS21C084
7942	17792	28032	1.49	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
7943	17793	28033	1.57	1.7E-01	AA627972.1	EST_HUMAN	trf0007.s1 NCL CGAP. C06 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gbl:26581
8007	17968	28208	9.13	1.7E-01	BC300355.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
8182	18068	28317	2.47	1.7E-01	AA314671.1	EST_HUMAN	60728647F1 NH1.MGC.44 Homo sapiens cDNA clone IMAGE:3613268 5'
8458	18335	28556	7.88	1.7E-01	7108300	NT	453a33.s1 NCL CGAP. C05 Homo sapiens cDNA clone IMAGE:1426924 3'
8458	18335	28559	2.88	1.7E-01	7108300	NT	Mus musculus chromatin polyoma cell binding protein Evt (Ebt1), mRNA
8458	18377	28559	2.88	1.7E-01	7108300	NT	Mus musculus chromatin polyoma cell binding protein Evt (Ebt1), mRNA
8458	18377	28559	2.88	1.7E-01	7108300	NT	AMP NUCLEOSIDASE
8012	18511	29107	4.38	1.7E-01	11418187	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1), mRNA
9139	19056		1.5	1.7E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9420	19513		1.28	1.7E-01	AB24404.1	EST_HUMAN	ACID RECEPTOR ALPHA-1 (HUMAN);
9705	19253	25218	5.79	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
120	10097	15917	1.88	1.8E-01	AF217632.1	NT	Homo sapiens mitogen-activated kinase gene, exon 6 and 7
664	12641	26416	1.53	1.8E-01	R31497.1	EST_HUMAN	Y107127.1 Scenara placenta Nucleo-PP Homo sapiens cDNA clone IMAGE:135896 5'
1605	11469	21288	4.08	1.8E-01	AF298177.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1882	11778	21663	2.4	1.8E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1941	11836		1	1.8E-01	U03344.1	NT	Caenorhabditis gigas RNA polymerase II target subunit mRNA, partial cds
2335	12719	22115	0.96	1.8E-01	X94282.1	NT	H. sapiens mRNA for novel T-cell activation protein
2443	12320	22218	2.19	1.8E-01	AB373720.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2863	12791	22593	8.9	1.8E-01	AF185689.1	NT	Homo sapiens cyclochrome P450 3A4 (CYP3A4) gene, promoter region
2963	12791	22594	8.9	1.8E-01	AF185689.1	NT	Homo sapiens cyclochrome P450 3A4 (CYP3A4) gene, promoter region
3351	13495	23285	1.31	1.8E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichedul AB3 gene
3351	13495	23286	1.31	1.8E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichedul AB3 gene
3391	13828		2.61	1.8E-01	AE304413.1	NT	Vario chlamydomonas II, section 70 of 93 of the complete chromosome

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4294	14132	23908	7.62	1.E-01	AJ179880.1	NT	Homo sapiens apelin gene, complete cds
4393	14249		2.44	1.E-01	AW958001.1	EST_HUMAN	EST330077 IMAGE reassessment, IMAGE Homo sapiens cDNA
4391	14267		4.01	1.E-01	E763319.1	NT	Mus musculus chaperitin subunit 3 (gaira) (Cdr), mRNA
4781	14695	24451	0.86	1.E-01	Z28330.1	NT	S cerealisae chromosome XJ reading frame ORF YKR103c
4781	14695	24452	0.86	1.E-01	Z28330.1	NT	S cerealisae chromosome XI reading frame ORF YKR103c
4865	14749	24524	1.14	1.E-01	AA088343.1	EST_HUMAN	28dH04 at Strathgoun colob (#637204) Homo sapiens cDNA clone IMAGE511381.3 similar to TR-E221065
4859	14765	24540	1.92	1.E-01	AJ009359.1	NT	E22-1955 33,952 BP SEQUENCE OF CHROMOSOME XV.;
4869	14769	24547	1.92	1.E-01	AJ006336.1	NT	Lycopersicon esculentum Real fragment 2, satellite region
4868	14833	24601	1.09	1.E-01	BC018707.1	EST_HUMAN	YAC89809 at NIH JGCG. R3 Homo sapiens cDNA clone IMAGE2049023 s similar to pAB161715
5390	15559	25102	3.12	1.E-01	AW197468.1	EST_HUMAN	TRYPTOPHAN-L-TRNA SYNTHETASE (HUMAN); pbX89657 Mmusculus (MOUSE)
5390	15606	25163	3.12	1.E-01	AW197468.1	EST_HUMAN	HYPOKETIN1L 127.6 KD PROTEIN; ;
5398	15717	25364	2.07	1.E-01	AF034716.1	NT	Rattus norvegicus COAT A Translucor binding protein asolon (cepal) gene, complete cds
5973	15776	25898	2.24	1.E-01	AL167168.2	NT	Anopheles gambiae DNA chromosome 4, contig fragment No. 84
5973	15776	25899	2.24	1.E-01	AL167168.2	NT	Anopheles gambiae DNA chromosome 4, contig fragment No. 84
6157	16151	26135	3.7	1.E-01	AW197215.1	EST_HUMAN	U1B-B12-spl-6-D-U1at NCI CGAP Subst Homo sapiens cDNA clone IMAGE:724418.3'
6562	16420	26612	1.84	1.E-01	AW1245350.1	EST_HUMAN	28222438, spittle NH, JMG-C7 Homo sapiens cDNA clone IMAGE:28222438.5'
6562	16472	26692	1.42	1.E-01	AJ3349.1	NT	Gentia cordifolia androgen receptor gene, partial exon
7197	17064	27254	1.99	1.E-01	Z09091.1	NT	S cerealisae chromosome X reading frame ORF YJR001w
7594	17416		1.7	1.E-01	B537617.1	EST_HUMAN	RG3-STO200-041199-011-H61 ST0200 Homo sapiens cDNA
7595	17416	27631	1.91	1.E-01	Z09091.1	NT	S cerealisae chromosome X reading frame ORF YJR001w
8048	17940	28100	2.71	1.E-01	AV18506363.1	EST_HUMAN	IJ3-CT0230-111192 G2B-GQI OT020 Homo sapiens cDNA
8394	18241	28460	1.78	1.E-01	O14647	SWISSPROT	CHROMODOMAINHELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
8394	18331	28461	1.78	1.E-01	O14647	SWISSPROT	CHROMODOMAINHELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
8459	18332		7.6	1.E-01	AI100604.1	NT	Pleurodictum fidiatum calcium-dependent protein kinase3 (cdsk3) gene, complete cds
8713	18538	28814	10.07	1.E-01	6671532	EST_HUMAN	Mus musculus adaptor-related protein complex AP-1, beta 1 isoform (Acr1b1), mRNA
9001	18804	29097	2.99	1.E-01	AW877427.1	EST_HUMAN	OY2-F7010-100400-133-a08 PT0010 Homo sapiens cDNA
9025	19876		2.17	1.E-01	6679466	EST_HUMAN	Mus musculus protein kinase, cAMP dependent, type II (Pka2), mRNA
9141	19878		1.96	1.E-01	AV1715655.1	EST_HUMAN	Quercus sativa K3 mRNA for anti-Laurene synthase, complete cds
9595	19953		6.33	1.E-01	AJ004495.1	NT	Homo sapiens mRNA for FLN0104 protein, partial cds
9727	19965		2.84	1.E-01	AK024469.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9807	18319		2.47	1.9E-01	AF287344.1	NT	Fuchsi hybrid culture Qia 94208 (ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product)
9827	19328	25208	1.27	1.9E-01	9506522	NT	Rat brain neurexin chondroitin sulfate proteoglycan 5 (neuroglycan C) (Csp65), mRNA
248	10214	20330	1.87	1.9E-01	BE710037.1	EST_HUMAN	L3-HIT0619-04-0700-197-E05 HT0619 Homo sapiens cDNA
248	10214	20331	1.87	1.9E-01	BE710037.1	EST_HUMAN	L3-HIT0619-04-0700-197-E05 HT0619 Homo sapiens cDNA
572	12640		2.28	1.9E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
769	10607	20534	1.4	1.9E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21 C084
1070	10992	20534	0.89	1.9E-01	AJ009735.1	NT	Oryzias caprip mRNA for EGG52 myosin heavy chain, 3'UTR
1097	11013	20638	1.87	1.9E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1188	11108	20693	1.36	1.9E-01	AW165516.1	EST_HUMAN	Rat brain neurexin chondroitin sulfate proteoglycan 5 (neuroglycan C) (Csp65), mRNA
1254	11181	21010	2.81	1.9E-01	D26893.1	NT	xx36011.x1 NCL CGAP K411 Homo sapiens cDNA clone IMAGE:2569088 3'
1254	11181	21011	2.81	1.9E-01	D26893.1	NT	xx36011.x1 NCL CGAP K411 Homo sapiens cDNA clone IMAGE:2569088 3'
1466	11371	21238	1.49	1.9E-01	AF117340.1	NT	Human gene for dihydropyrimidinase complete cds (exon 1-5)
1868	11762	21698	1.54	1.9E-01	AW144451.1	EST_HUMAN	Mus musculus MAP kinase kinase kinase 1 (Mkk1) mRNA, complete cds
2079	12544	22435	1.12	1.9E-01	BF603931.1	EST_HUMAN	80208326F1 NH_MGC_81 Homo sapiens cDNA clone IMAGE:2733941 3'
2899	12927	22716	0.89	1.9E-01	NP1441.1	NT	Box lacunae factor V (partial 2' (5' to 3') YmRNA, complete cds
3308	13229	23034	4.22	1.9E-01	AA693049.1	EST_HUMAN	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN);
3322	13242	23048	0.87	1.9E-01	Z3104.1	NT	L. tagalensis mRNA for G protein-coupled receptor
3322	13242	23049	0.87	1.9E-01	Z3104.1	NT	L. tagalensis mRNA for G protein-coupled receptor
3380	13298	23067	0.89	1.9E-01	AW612237.1	EST_HUMAN	hG0002.N1 NCL CGAP Luc4 Homo sapiens cDNA clone IMAGE:2565539 3' similar to contains element MER10 repetitive element;
3908	13610	23394	1.34	1.9E-01	U06964.1	NT	Mus musculus C19orf56 glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	13619	23403	185.26	1.9E-01	71085938	EST_HUMAN	Homo sapiens pyruvate dehydrogenase kinase, isoform 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3751	13703	23400	2.35	1.9E-01	AW195993.1	NT	h10065.x1 Soares, NH_T, GBC, S11 Homo sapiens cDNA clone IMAGE:2981411 3'
3906	13718	23503	0.8	1.9E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal AB3 gene
3806	13718	23507	0.8	1.9E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal AB3 gene
3904	13871	23648	0.99	1.9E-01	AW195959.1	EST_HUMAN	RQ2-HIT0149-191059-012-509 HT0149 Homo sapiens cDNA
4005	13872	23687	0.97	1.9E-01	Z12323.1	NT	B. napus mitochondrial DNA for ORF158
4001	13961	23768	8.36	1.9E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21 C084
4623	14511	24301	1.34	1.9E-01	BF607695.1	EST_HUMAN	802067102F1 NH_MGC_57 Homo sapiens cDNA clone IMAGE:4068223 5'

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4846	12644	22436	2.18	1.8E-01	BF60381.1	EST_HUMAN	180238299P1 NH1_MGC_34 Homo sapiens cDNA clone IMAGE:4247537 5'
4880	14566	24361	1.08	1.8E-01	BE173796.1	EST_HUMAN	CN0-HT0695-280200-245-610 HT0586 Homo sapiens cDNA
4880	14566	24362	1.08	1.8E-01	BE173796.1	EST_HUMAN	CN0-HT0695-280200-245-610 HT0586 Homo sapiens cDNA
4929	14508	24576	1.3	1.8E-01	AL191650.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5072	14942	24716	0.94	1.8E-01	AF003105.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds
5216	16139	24833	2.02	1.8E-01	H07969	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5269	15183		5.97		P15190	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX 3-TEROID-BINDING PROTEIN)
5400	18319	25967	4.08	1.8E-01	AW55074.1	EST_HUMAN	L3-CT0219-180200-064-F10 CT0219 Homo sapiens cDNA
5424	18346	26368	6.77	1.8E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGF α) mRNA, complete cds
5424	18346	26368	6.77	1.8E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGF α) mRNA, complete cds
5652	15564	25661	1.9	1.8E-01	6738669	NT	Mus musculus DNA methyltransferase 2 (Dnmt2) mRNA
5652	15564	25661	1.9	1.8E-01	6738669	NT	Mus musculus DNA methyltransferase 2 (Dnmt2) mRNA
5694	15563	25694	4.97	1.8E-01	AL278625.1	NT	Mus musculus genomic fragment, 279 kb, chromosome 7
5780	15568	26774	2.44	1.8E-01	BE277653.1	EST_HUMAN	B0154322F1 NH1_MGC_20 Homo sapiens cDNA clone IMAGE:3553981 5'
5780	15568	26774	2.44	1.8E-01	BE277653.1	EST_HUMAN	Homo sapiens RAD51 (S. cerevisiae) homolog (RAD51L) mRNA
5828	16734	25845	1.78	1.8E-01	AF154007.1	NT	Influenza B virus (B/Nanchang/490/94) NP protein, gene, complete cds, and neuraminidase gene, partial cds
5917	16465	23346	1.98	1.8E-01	AE010361.1	NT	Archaeoglobus fulgidus actin, 88 of 172 of the complete genome
5958	16540	25963	6.13	1.8E-01	11417238	NT	Homo sapiens chromosome 5 open reading frame 3 (COR3), mRNA
5942	16447	26971	1.81	1.8E-01	AF4808	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-LC) (GCS LIGHT CHAIN)
5972	16579	26000	2.09	1.8E-01	Q26462	SWISSPROT	HYPOPHOSPHATASE 1/7 KD PROTEIN IN THRO-1/2B INTERGENIC REGION (ORF8)
6031	16595	26067	1.4	1.8E-01	P50743	SWISSPROT	AMINOGLUCONAMINIDASE
6108	16123	24966	6.93	1.8E-01	AW070296.1	EST_HUMAN	HYPOPHOSPHATASE 1/7 KD PROTEIN IN THRO-1/2B INTERGENIC REGION (ORF8)
6284	16148		1.77	1.8E-01	AW070296.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6374	16250	26360	1.88	1.8E-01	AF070492.1	EST_HUMAN	wf0208.x1 NO1_GGAP UHT Homo sapiens cDNA clone IMAGE:2461310 3'
6481	16340	26507	1.98	1.8E-01	AF070492.1	EST_HUMAN	UHFH-BNG-alk-305-Q1-7 NH1_MGC_60 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26508	1.98	1.8E-01	AF070492.1	EST_HUMAN	UHFH-BNG-alk-305-Q1-7 NH1_MGC_60 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26508	1.98	1.8E-01	AF070492.1	EST_HUMAN	UHFH-BNG-alk-305-Q1-7 NH1_MGC_60 Homo sapiens cDNA clone IMAGE:3077409 5'
6765	16566	26999	1.22	1.8E-01	AA870317.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN)
6895	16774		1.77	1.8E-01	CE16900.1	EST_HUMAN	CT18800 Cerebellar human actin polyA+ mRNA (18807) Homo sapiens cDNA clone GEN-629109 5'
6912	16790	26983	1.88	1.8E-01	L27835.1	NT	Pangasinan-induced gliosis growth hormone (GH) mRNA, complete cds
6965	16573	27064	1.44	1.8E-01	D84476.1	NT	Homo sapiens mRNA for ASK1, complete cds

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Table 4

Probe SEQ ID NC:	Exon SEQ ID	ORF SEQ ID NC:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accuscion No.	Top Hit Database Source	Top Hit Descriptor
2782	12624	23517	3.07	1.4E-01	A0363466.1	EST_HUMAN	wnt74drt.lx1.NCI_GGAP_U02 Homo sapiens cDNA clone IMAGE:2441866 ³
3823	43736	23524	1	1.4E-01	R65932.1	EST_HUMAN	yfrtad03.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:41467 ⁵
3823	43736	23526	1	1.4E-01	R65932.1	EST_HUMAN	yfrtad03.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:41467 ⁵
4083	43395	23762	8.38	1.4E-01	A056204.1	EST_HUMAN	yfrtad02.x1 NCI_GGAP_Luz21 Homo sapiens cDNA clone IMAGE:2279570 ³
4083	43395	23763	8.38	1.4E-01	A056204.1	EST_HUMAN	yfrtad02.x1 NCI_GGAP_Luz21 Homo sapiens cDNA clone IMAGE:2279570 ³
4144	14044	23817	3.16	1.4E-01	AE001710.1	NT	Theomedia malina strain 22 of 135 of the complete genome
4313	14210		0.8	1.4E-01	AA772937.1	EST_HUMAN	p90041.a1 Soares fetal liver spleen, INFELS S1 Homo sapiens cDNA clone IMAGE:455973 ³ similar to p9-X01057, just INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element
6032	14904		0.91	1.4E-01	AV086022.1	EST_HUMAN	OJ3.SN0022.100550-185-Hop UNK022 Homo sap eare cDNA
5165	14984	24769	1	1.4E-01	AL152384.2	NT	Homo sapiens chromosome 21, experiment HS21.0384
5165	15074	24764	0.81	1.4E-01	X000160.1	NT	Y-japanesec ecumulum genomes R4P0 band 26
5248	15171	24944	4.5	1.4E-01	I193777.1	EST_HUMAN	yf0511.s1 Stragelung lung (R57210) Homo sapiens cDNA clone IMAGE:111812 ³
5267	16189	24983	4.29	1.4E-01	A0500455.1	NT	Candida tropicalis DNA for mitochondrial NAOP-linked isozyme dehydrogenase, complete cds
5387	16769	24984	4.29	1.4E-01	A0500455.1	NT	Candida tropicalis DNA for mitochondrial NAOP-linked isozyme dehydrogenase, complete cds
5905	15710	25923	2.72	1.4E-01	SC323891.1	EST_HUMAN	yfrt02.d2.x1 NCI_GGAP_A011 Homo sapiens cDNA clone IMAGE:3133338 ³
5905	15809	25934	5.94	1.4E-01	AU117147.1	EST_HUMAN	AU117147.1 HEMBA1 Homo sapiens cDNA clone HEIMBA1000769 ⁵
5903	15803	25935	5.94	1.4E-01	AU117147.1	EST_HUMAN	AU117147.1 HEMBA1 Homo sapiens cDNA clone HEIMBA1000769 ⁵
5958	15893	25965	3.07	1.4E-01	AV01082798.1	EST_HUMAN	x071d12.x1 Soares, NFL_T_3BC S1 Homo sapiens cDNA clone IMAGE:3537381 ⁵
5959	15874		1.56	1.4E-01	SC205346.1	EST_HUMAN	QV1195323F.NHL_MGC_7 Homo sapiens cDNA clone IMAGE:2381767 ³
5962	15887	230019	1.89	1.4E-01	BF378533.1	EST_HUMAN	QV1195323F.NHL_MGC_7 Homo sapiens cDNA clone IMAGE:2381767 ³
6371	16233		1.62	1.4E-01	AV015673.1	EST_HUMAN	UHH-B04047.GLC Homo sapiens cDNA clone GLC-FHS09.3
6536	16814		1.33	1.4E-01	AV055947.1	EST_HUMAN	HEB05047.GLC Homo sapiens cDNA clone GLC-FHS09.3
7167	17044	27236	4.48	1.4E-01	N3307073.1	EST_HUMAN	EST178102.Cabin carcinoma (HCCO) cell line Homo sapiens cDNA 5' end
7300	17178	27371	8.08	1.4E-01	SF310369.1	EST_HUMAN	EST178102.Cabin carcinoma (HCCO) cell line Homo sapiens cDNA 5' end
7343	17271		1.36	1.4E-01	W09411.1	EST_HUMAN	x08A04.r1 Soares, fetal heart, NHFH19W Homo sapiens cDNA clone IMAGE:351102 ⁵ similar to contains element KCR, repetitive element
7387	17266	27461	1.88	1.4E-01	Y101061.1	NT	Homo sapiens PHEX gene
7387	17266	27462	1.86	1.4E-01	Y101061.1	NT	Homo sapiens PHEX gene
7436	16449	26859	2.03	1.4E-01	AF121361.1	NT	Oncophila melanogaster signal transducing adaptor protein (STAMP), serine threonine kinase la (ATL), and zinc finger protein (DNZ1) genes, complete cds
8091	17682		2.02	1.4E-01	AF1481480.1	EST_HUMAN	zinc finger protein (DNZ1) genes, complete cds
8216	18100	28352	3.28	1.4E-01	R33400.1	EST_HUMAN	AB043631.1 NCI_GGAP_CGB1 Homo sapiens cDNA clone IMAGE:1320384 ³
8713	18490	28751	1.89	1.4E-01	X936302.1	NT	yfrtad01.r1 Soares breast ZNH3Bat Homo sapiens cDNA clone IMAGE:154988 ⁵
8916	18400		1.99	1.4E-01	X936302.1	NT	C-jun/cJun are BRF for putative membrane transport protein

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8764	17913	28108	2.23	1.4E-01	U28780.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TFI) genes, complete cds
8813	18626		3.02	1.4E-01	X62102.1	NT	M. musculus p18k gene for 18 kDa protein
9365	19517	25138	1.48	1.4E-01	AB000690.1	NT	Erythrina flavellata mRNA for adhesion, partial cds
9413	19065	25277	2.32	1.4E-01	X74773.1	NT	P. salinus plantid gene seq
9427	19073		1.89	1.4E-01	11688117	NT	Rattus norvegicus domain (Dns), mRNA
9470	19724		1.82	1.4E-01	BC613602.1	EST_HUMAN	801315038F1 NH, MGCC 8 Homo sapiens cDNA clone IMAGE383429 5'
9590	19165		3.01	1.4E-01	AF083221.1	NT	Fugu ubitripes putative neurotransmitter receptors, YDR140W homolog, and glycinamide ribonucleotide transferase (GART) genes, complete cds
9573	19163		2.29	1.4E-01	D64004.1	NT	Synchytrium sp. PC65803 complete genome, 2327, 28957-300285
9646	19744		3.28	1.4E-01	P10447	SWISSPROT	TYROSINE PROTEIN KINASE TRANSFORMING PROTEIN ABL
9762	19232		1.41	1.4E-01	BE782738.1	EST_HUMAN	80146575F1 NH, MGCC 67 Homo sapiens cDNA clone IMAGE383765 5'
9831	19332		1.42	1.4E-01	11426031	NT	Homo sapiens echin-83 (EFN83), mRNA
9850	19595		3.41	1.4E-01	D62983.1	NT	Mus musculus mRNA for prolactin, complete cds
9828	19398		1.77	1.4E-01	AV1377968.1	EST_HUMAN	MF04110206.221293-204-48117028 Homo sapiens cDNA
319	10231	20068	2.69	1.3E-01	4759467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	10231	20069	2.69	1.3E-01	4759467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	10460	20271	1.85	1.3E-01	AB013193.1	NT	Homo sapiens gene for NBS1, complete cds
620	10557	20369	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Gillington/93UK RNA for capsid protein (ORF2), strain HUNLV/Gillington/93UK
620	10557	20370	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Gillington/93UK RNA for capsid protein (ORF2), strain HUNLV/Gillington/93UK
626	10783	20503	1.09	1.3E-01	X63330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
876	10802	20662	1.83	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	10928	20771	1.55	1.3E-01	AL117078.1	NT	Borrelia burgdorferi strain T4 cDNA library under conditions of nitrogen deprivation
1111	11028		2.23	1.3E-01	AL116295.1	NT	Borrelia burgdorferi strain T4 cDNA library under conditions of nitrogen deprivation
1197	11107	20962	1.07	1.3E-01	AV171497.1	EST_HUMAN	AV171497 DCA Homo sapiens cDNA clone DCAA7-75 5'
1426	11331		1.38	1.3E-01	AF149277.1	NT	Homo sapiens adipeal protein cDNA mRNA, complete cds
1916	11811	21689	2.58	1.3E-01	AL117078.1	NT	Borrelia burgdorferi strain T4 cDNA library under conditions of nitrogen deprivation
2124	12012		1.29	1.3E-01	AJ283578.1	NT	Rhodospirillum rubrum scd3pH8, pucA5, pucA6, pucA7, pucA8, pucA9 and pucC genes and ORF191
2245	12129		1.17	1.3E-01	AV1812104.1	EST_HUMAN	RC4-ST0175-191058-032-412 ST0173 Homo sapiens cDNA
2329	12210		2.99	1.3E-01	AE001018.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2542	12419	22305	3.49	1.3E-01	M69618.1	NT	Canis lupus familiaris keratin type I mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3404	13321	23122	0.95	1.3E-01	M21972.1	NT	Bovine branched chain alpha-keto acid dihydrolipoic transacylase mRNA, complete cds
3601	13575	23362	1.18	1.3E-01	AF000001.1	NT	Pyrococcus horkeshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3951	13575	23363	1.18	1.3E-01	AF000001.1	NT	Pyrococcus horkeshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3957	13581	23368	0.78	1.3E-01	AF000001.1	NT	Pyrococcus DDI gene for dihydrodihydroxyase 4 (AKR-1C4) exon 2
3714	13575	23362	0.96	1.3E-01	AF000001.1	NT	Pyrococcus horkeshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3714	13575	23363	0.96	1.3E-01	AF000001.1	NT	Pyrococcus horkeshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3734	13649	23431	0.85	1.3E-01	6078940	NT	Rattus norvegicus Flavinogen, gamma polypeptide (F3g), mRNA
3906	13616	23431	1.7	1.3E-01	AL161591.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4066	13948		1.15	1.3E-01	AF020713.1	NT	Bacteriophage SPB-2 complete genome
4066	13968		3.44	1.3E-01	AF034411.1	EST_HUMAN	QV3-DT0018-081258-036-03 DT0018 Homo sapiens cDNA
4075	13971	23755	1.69	1.3E-01	AF028905.1	NT	Schistosoma mansoni fructose bisphosphate aldolase mRNA, complete cds
4083	13993	23770	16.36	1.3E-01	AF027341.1	EST_HUMAN	Y2310.11 Scores, NFI, T, C8C, S1 Homo sapiens cDNA clone IMAGE:2813956 3'
4192	14092	23870	0.85	1.3E-01	AF075227.1	EST_HUMAN	AV752278 NPD Homo sapiens cDNA clone NPDAZ502 5'
4192	14092	23871	0.85	1.3E-01	AF075227.1	EST_HUMAN	AV752278 NPD Homo sapiens cDNA clone NPDAZ502 5'
4216	14119		1.65	1.3E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C083
4433	14328	24116	2.08	1.3E-01	AF0272380.1	EST_HUMAN	60715305F1 NH1.MGC_83 Homo sapiens cDNA clone IMAGE:256003 5'
4525	14348	24202	0.81	1.3E-01	AF070643.1	EST_HUMAN	60715305F1 NH1.MGC_83 Homo sapiens cDNA clone IMAGE:256003 5'
4771	15078		3.17	1.3E-01	AF084017.1	EST_HUMAN	60715305F1 NH1.MGC_71 Homo sapiens cDNA clone IMAGE:3511387 5'
4803	14783		0.86	1.3E-01	AF153594.2	NT	AL138619 PLAGE1 Homo sapiens cDNA clone FLAGE104053 5'
5074	14944	24716	1.21	1.3E-01	AL153284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5074	14944	24716	1.21	1.3E-01	AL153284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5173	15039	24805	0.9	1.3E-01	AF070619.1	EST_HUMAN	60715305F1 NH1.MGC_83 Homo sapiens cDNA clone IMAGE:256003 5'
5173	15039	24805	0.9	1.3E-01	AF070619.1	EST_HUMAN	60715305F1 NH1.MGC_83 Homo sapiens cDNA clone IMAGE:256003 5'
5202	15273	25073	2.51	1.3E-01	AF080417.1	EST_HUMAN	QV140005-100400-189-405 U00055 Homo sapiens cDNA
5428	15348		1.79	1.3E-01	AF036680.1	NT	Hepatitis C virus 69, C110 genome polyprotein gene, partial cds
5504	15510	25506	13.21	1.3E-01	AF031330.1	NT	Schistosoma chromocytoma pombe gene for Alp41, complete cds
5546	15991	25963	2.04	1.3E-01	X89891.1	NT	Schistosoma chromocytoma pombe gene for Alp41, complete cds
6305	16169		2	1.3E-01	HA0994.1	EST_HUMAN	Y53402.1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207076 5'
6549	16529	26723	1.34	1.3E-01	11423284	NT	Homo sapiens PRO0811 protein (PRO0811), mRNA
6598	16548	26744	1.28	1.3E-01	BF060522.1	EST_HUMAN	602187015T1 NH1.MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
6598	16737		4.54	1.3E-01	Z71102.1	NT	S. cerevisiae chromosome IV reading frame ORF YD_054c
8895	16795		4.14	1.3E-01	8623919	NT	Homo sapiens core histone H2A2.2 (H2A2.2) mRNA
8900	16836	27031	1.27	1.3E-01	BF060522.1	EST_HUMAN	602187015T1 NH1.MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
7452	17291	27407	4.45	1.3E-01	AF023129.1	NT	Oryzabagrus caricatus H2-K-A1Pase alpha 2c subunit mRNA, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8025	17621		2.88	1.3E-01	BF330999.1	EST_HUMAN	MF4-471038-130700-0108 B10388 Homo sapiens cDNA
8444	18318	28577	1.83	1.3E-01	AF119171.1	NT	Homo sapiens Apoptamine transporter (SLC6A3) gene, complete cds
8576	18444		6.13	1.3E-01	6671745	NT	Mus musculus collagen 2, muscle (COL2), mRNA
8873	18685	28676	3.72	1.3E-01	BE27049.1	EST_HUMAN	R0118902F1 NIH_MGC_27 Homo sapiens cDNA clone IMAGE:3604804 5'
9291	18686	29320	1.97	1.3E-01	BE108346.1	EST_HUMAN	80146274F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:386003 5'
9369	19054		3.18	1.3E-01	AJ242790.1	NT	Gallus gallus sox1 gene for lymphoblasts, exons 1-3
9757	19279		1.56	1.3E-01	AB023629.1	NT	Epiphyas fluitellus mRNA, for sALC-6, complete cds
9764	19297		1.32	1.3E-01	AW001114.1	EST_HUMAN	WU2409.X1 Sources: Disclorale, colon, NHCO Homo sapiens cDNA clone IMAGE:2520377 3' similar to TR-O6287
9945	19414		1.26	1.3E-01	BF571784.1	EST_HUMAN	TR-O6287 O6287 KIA00639 PROTEIN. ;
378	10362	20185	7.21	1.2E-01	AI421744.1	EST_HUMAN	IG3602.X1 NCL_GCAP_Bnc23 Homo sapiens cDNA clone IMAGE:2086339 3' similar to gbAU06760_m1
418	5685		1.55	1.2E-01	U66912.1	NT	ANNEXXIN V (HUMAN);
635	10476		2.93	1.2E-01	AF30942.1	NT	Dicystellum discoideum ORF DG1016 gene, partial cds
1335	11281	21117	2.78	1.2E-01	AI149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-48 mRNA, partial cds
1335	11281	21118	2.78	1.2E-01	AI149146.1	EST_HUMAN	AU149146.X1 NT78M4 Homo sapiens cDNA clone NT78M4001691 3'
1381	11297		3.94	1.2E-01	AI758249.1	EST_HUMAN	AU149146.X1 NT78M4 Homo sapiens cDNA clone NT78M4001691 3'
1460	11395		1.13	1.2E-01	AA897474.1	EST_HUMAN	AF35236 cDNA Homo sapiens cDNA clone cDNA1.B1.5'
1613	11517	21377	1.17	1.2E-01	C14634	SWISSPROT	af89c9.x1 Sources: NEI, T_GSC S1 Homo sapiens cDNA clone IMAGE:146954 3' similar to TR-Q16871
1631	11535	21396	2.52	1.2E-01	AI265402.1	EST_HUMAN	Q16871 ANTIMULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR ;
1750	11631		28.48	1.2E-01	X69211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOSOLIC 4 (T CELL TRANSCRIPTION FACTOR
1877	11773		1.43	1.2E-01	AW446988.1	EST_HUMAN	Q6909.X1 NCL_GCAP_E502 Homo sapiens cDNA clone IMAGE:1900583 3'
2134	12022	21919	2.1	1.2E-01	BF246480.1	EST_HUMAN	U14883.X1 NCL_GCAP_E502 Homo sapiens cDNA clone IMAGE:274454 3'
2240	12124	22026	1.01	1.2E-01	AI163213.2	NT	U14883.X1 NCL_GCAP_E502 Homo sapiens cDNA clone IMAGE:274454 3'
2546	12420	22310	2.02	1.2E-01	AW399556.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21.D013
2697	12561	22451	0.68	1.2E-01	AK23388.1	EST_HUMAN	QV3-BN0046-220300-129-110 BN0046 Homo sapiens cDNA
2812	12741	22537	1.5	1.2E-01	U18018.1	NT	hs19697.X1 NCL_GCAP_Pant1 Homo sapiens cDNA clone IMAGE:222888 3' similar to TR-Q14048 Q14048
2874	12799	22564	1.96	1.2E-01	A1720470.1	EST_HUMAN	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN, [1] contains element P1785 negative element ;
2901	12831	22628	2.88	1.2E-01	M16394.1	NT	Human E1A enhancer binding protein (E1A-F) mRNA, partial cds
							hs00009.X1 Barstarad colon HPL1877 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gbL06095
							805 REBSONAL PROTEIN L30 (HUMAN);
							Human crestinol kinase-B mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2074	12601	22700	0.98	1.2E-01	X59882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3192	13117	22923	2	1.2E-01	AV1376038.1	EST_HUMAN	QY1-317028-261089-021-005 B10259 Homo sapiens cDNA
3219	13143	22923	0.97	1.2E-01	U07600.1	EST	Methanococcus jannaschii section 142 of 150 of the complete genome
3433	13350	23108	0.79	1.2E-01	D20118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2796131 to 30113540
3477	13303	23108	1.14	1.2E-01	X59882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3477	13303	23108	1.14	1.2E-01	X59882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3554	13350	23108	1.14	1.2E-01	X59882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3704	13617	23706	0.86	1.2E-01	U07600.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21): from 2796131 to 30113540
4090	13900	23706	2.2	1.2E-01	U07600.1	EST_HUMAN	6018107681 NH ₂ MGCC 48 Homo sapiens cDNA clone IMAGE:4036583
4090	13900	23706	2.2	1.2E-01	U07600.1	EST_HUMAN	6018107681 NH ₂ MGCC 48 Homo sapiens cDNA clone IMAGE:4036583
5012	14898	23707	2.2	1.2E-01	U07600.1	EST_HUMAN	P. claudii mRNA, repeat region (ID 218177)
5174	16540	24827	1.04	1.2E-01	P16496	SWISSPROT	HEMOXYLIN PRECURSOR
5174	16540	24827	1.47	1.2E-01	U00441	SWISSPROT	HYPOHETICAL 82.4 KD PROTEIN C12B10.082 IN C-HROMOSOME 1
5174	16540	24827	1.47	1.2E-01	U00441	SWISSPROT	HYPOHETICAL 82.4 KD PROTEIN C12B10.082 IN C-HROMOSOME 1
5189	15002	24827	2.47	1.2E-01	U00441	EST_HUMAN	UHF-BKG-anti-501-ULT NH ₂ MGCC 38 Homo sapiens cDNA clone IMAGE:305817.6
5251	15174	25021	2.83	1.2E-01	U07600.1	EST_HUMAN	UHF-BKG-anti-501-ULT NH ₂ MGCC 38 Homo sapiens cDNA clone IMAGE:321099.5
5257	15218	25021	1.19	1.2E-01	U07600.1	EST_HUMAN	UHF-BKG-anti-501-ULT NH ₂ MGCC 38 Homo sapiens cDNA clone IMAGE:321099.5
5762	15099	25776	1.69	1.2E-01	U07600.1	EST_HUMAN	Homo sapiens gene encoding pleiotrophin (ecton 1-13)
5908	15711	25824	2.19	1.2E-01	U07600.1	EST_HUMAN	U07600.1-221068-113-004 C10031 Homo sapiens cDNA
5939	15745	25949	1.58	1.2E-01	U07600.1	EST_HUMAN	Mouse glucocorticoid-induced mRNA, complete cds
6007	15437	25949	1.21	1.2E-01	U07600.1	EST_HUMAN	Mouse glucocorticoid-induced mRNA, complete cds
6842	15622	28715	2.46	1.2E-01	AF191763.1	EST_HUMAN	W09603.x1 NOL_OGAP_C03 Homo sapiens cDNA clone IMAGE:2326804.3 similar to SW-GST2_HUMAN
6893	16772		9.72	1.2E-01	AF083652.1	EST_HUMAN	Q09795 MICROSMAL GLUTATHIONE S-TRANSFERASE II; jc6d407.x1 NOL_OGAP_E02 Homo sapiens cDNA clone IMAGE:2887997.3 similar to glnM13452 LAMIN A (HUMAN);
6904	16782		3.89	1.2E-01	AF083772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombination (sin) gene, partial cds; and transcriptional regulator QseR (qseR) and multidrug efflux protein QseF (qseF) genes, complete cds
7043	16920		2.27	1.2E-01	U07600.1	NT	Haemophilus influenzae Rd section 29 of 153 of the complete genome
7521	17340	27548	1.5	1.2E-01	U07600.1	NT	S. cerevisiae HXT15 gene
7747	17597	27819	1.51	1.2E-01	AF170857.1	EST_HUMAN	AF170857 Cui Homo sapiens cDNA clone CuiAXE08.5
8290	18140		2.95	1.2E-01	D23184.1	NT	Yeast MF15 gene for suppressor protein, complete cds
8417	18201		3.35	1.2E-01	U07600.1	EST_HUMAN	6016555781 NH ₂ MGCC 65 Homo sapiens cDNA clone IMAGE:344283.3
8487	18300		1.93	1.2E-01	U07600.1	EST_HUMAN	6019007031 NH ₂ MGCC 19 Homo sapiens cDNA clone IMAGE:4130103.5
8579	18447	28715	2.6	1.2E-01	AF190463.1	NT	Homo sapiens dyx11 intermediate chain DNAT1 (DNAT1) gene, exon 17

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8798	18812		2.02	1.2E-01	M55106.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
9032	18822		2.22	1.2E-01	AF569033.1	EST_HUMAN	AF569033 GLIO Homo sapiens cDNA clone GLCPB12 3'
9383	19043		2.78	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudobisnormal region, segment 2/2
9459	19583	24857	2.58	1.2E-01	Q64912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
9671	10476		7.59	1.2E-01	AF339442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
9671	19220		1.41	1.2E-01	X53951.1	NT	R. norvegicus NF68 gene for c8bDa neurofilament
9739	19708	24903	2.35	1.2E-01	BE061418.1	EST_HUMAN	OV44T0234-11109-031-c10 BT0234 Homo sapiens cDNA
9761	19281	25231	3.68	1.2E-01	AL268003.1	EST_HUMAN	902005.x1 NCL CGAP Lu5 Homo sapiens cDNA clone IMAGE1868940 3'
9782	19295		2.07	1.2E-01	L0187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
9786	19356		4.72	1.2E-01	C98433	SWISSPROT	CYC1IN 1
9880	19424		2.19	1.2E-01	AF531448.1	EST_HUMAN	h18268.x1 NCL CGAP Bc28 Homo sapiens cDNA clone IMAGE2167983 5'
992	10493	20301	0.96	1.1E-01	AB61003.1	EST_HUMAN	h18268.x1 NCL CGAP Bc28 Homo sapiens cDNA clone IMAGE2167983 5'
889	10355	20344	3.38	1.1E-01	AA569038.1	EST_HUMAN	h18268.x1 NCL CGAP Bc28 Homo sapiens cDNA clone IMAGE2167983 5'
1038	10356	20780	1.63	1.1E-01	BF597308.1	EST_HUMAN	HEME OXYGENASE 1 (HMOX1)
1089	10885		1.29	1.1E-01	AL161560.2	NT	h18268.x1 NCL CGAP Bc28 Homo sapiens cDNA clone IMAGE2167983 5'
1143	12858	20858	4.08	1.1E-01	AF167158.1	EST_HUMAN	Acetabularia Indiana DNA chromocore 4, centig fragment NO. 60
1259	11137	20650	1.72	1.1E-01	D64004.1	NT	EST3304142 IMAGE2167983 complete genome 2027, 2988787-502865
1504	11408	21287	2.47	1.1E-01	AU140383.1	EST_HUMAN	Synovial cells up. PC58593 complete genome 2027, 2988787-502865
2066	12180		2.25	1.1E-01	6795216	NT	AU140383 FLA2c2 Homo sapiens cDNA clone PLACE2000403 5'
2462	12653		1.17	1.1E-01	6795216	NT	Mus musculus lre T-cell antigen receptor alpha (Ptra), mRNA
2520	12394		1.17	1.1E-01	AF1821906.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (CQ24), mRNA
2825	12754	22648	1.84	1.1E-01	AF521818.1	EST_HUMAN	ROD5-10378-210100-032-gp4 S10379 Homo sapiens cDNA
2967	12925	22717	0.8	1.1E-01	F03265.1	EST_HUMAN	Interleukin-12 p35 subunit (mice, Genomic, 700 nt, segment 4 of 5)
3269	13221	23082	1.39	1.1E-01	6793221	EST_HUMAN	HSC-1R222 normalized infant brain cDNA Homo sapiens cDNA clone c-1102 3'
3374	13253	23082	3	1.1E-01	BS338186.1	EST_HUMAN	Mus musculus celastrol chemel, voltage-dependent, T type, alpha 1G subunit (Ca _v 1.1g), mRNA
3405	13322	23123	1.54	1.1E-01	X32135.1	NT	h18268.x1 NCL CGAP Bc28 Homo sapiens cDNA clone IMAGE2167983 5'
3534	13450	23246	0.94	1.1E-01	Y07695.1	NT	Cranialdial nuclear gene on linkage group XIX
3648	13582	23348	1.23	1.1E-01	X52708.1	NT	A. thaliana gene for transposase
4021	13925	23658	1.31	1.1E-01	AF161942.1	EST_HUMAN	G. gallus gene encoding non-Histone chromosomal protein HMG-14b, exons 4 and 5
4021	13925	23659	1.31	1.1E-01	AF161942.1	EST_HUMAN	h18268.x1 NCL CGAP Bc28 Homo sapiens cDNA clone IMAGE2167983 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Signal	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7228	17165	27264	2.24	1.1E-01	A1492183.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
7228	17165	27265	2.24	1.1E-01	A1492183.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
7287	17163	27362	2.48	1.1E-01	U72873.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
7467	17327		2.08	1.1E-01	BF085149.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
7661	17371		1.23	1.1E-01	RG60590.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8181	18265	22717	1.84	1.1E-01	F03285.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8294	18173		3.88	1.1E-01	A149932.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8402	18276	26630	2.83	1.1E-01	R23706.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8519	18361	26635	1.95	1.1E-01	X71805.1	NT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8539	18411	28076	3.21	1.1E-01	U17610.1	NT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8538	18411	28077	3.21	1.1E-01	U17610.1	NT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8626	18401	28763	2.79	1.1E-01	P17437	SWISSPROT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8241	18060		3.19	1.1E-01	BE2767023.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
9465	19057		2.08	1.1E-01	BE674566.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
8663	18372	27592	2.14	1.1E-01	BF239763.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
1183	11154		4.08	1.0E-01	O62865	SWISSPROT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
1261	11958	21007	1.88	1.0E-01	A96409.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
1370	12176	21132	2.88	1.0E-01	U1416342.1	NT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
2438	12316	22213	1	1.0E-01	A14745355.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
3468	13364	23168	0.98	1.0E-01	A14745355.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
3658	13572	23359	2.01	1.0E-01	BF238918.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
3871	13782	23574	1.44	1.0E-01	BF238918.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
4307	14204	23637	1.5	1.0E-01	A14762346.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
4455	14348		1.17	1.0E-01	A14762346.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
4613	14731	24298	1.26	1.0E-01	U50450.1	NT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
4838	14719	24502	2.06	1.0E-01	A14662344.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
5188	15052	24782	0.87	1.0E-01	D46831.1	NT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
5188	15051	24615	1.44	1.0E-01	BF519635.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
5200	15590		9.16	1.0E-01	U66400.1	EST_HUMAN	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'
5270	15590	26630	11.21	1.0E-01	A7274875.1	NT	apb312.1 Stratiogene muscle 87/230 Homo sapiens cDNA clone IMAGE:627143.5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6187	18072		1.88	1.0E-01	U23821.1	EST_HUMAN	yf4-406.1 Scores placenta N52 P Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element
6549	16407		2.46	1.0E-01	U12488.1	NT	M. musculus with gene
7259	17175	27376	1.16	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synonym mRNA, complete cds
7473	17333		1.8	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7505	17293		2.73	1.0E-01	AE01601.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
7551	17501	27724	1.84	1.0E-01	BF240154.1	EST_HUMAN	801905551F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133497 5'
7713	17563	27798	9.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
7918	17768	27789	9.09	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
8050	17941	28007	1.26	1.0E-01	BE762750.1	EST_HUMAN	U158400AF1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3330596 5'
8393	18269	28520	2.9	1.0E-01	AL158127.1	EST_HUMAN	AU158127 THYRO1 Homo sapiens cDNA clone THYRO1000958 5'
8393	18269	28520	2.9	1.0E-01	BF240346.1	EST_HUMAN	801877703F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4106089 5'
8703	18321	28603	4.43	1.0E-01	BF240346.1	EST_HUMAN	801877703F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4106089 5'
8703	18321	28603	4.43	1.0E-01	BE760543.1	EST_HUMAN	801862556F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:394724 5'
9228	19385		2.5	1.0E-01	BE537719.1	EST_HUMAN	801065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:341633 5'
9453	19095		1.34	1.0E-01	U23821.1	NT	Homo sapiens KIAA0514 gene product (KIA0514), mRNA
9459	19098		2.03	1.0E-01	X08354.1	NT	Drosophila melanogaster ltr gene
9755	19098		2.57	1.0E-01	U23821.1	NT	Gonyaulax polyactis putative type-1 serine/threonine phosphatases (PF1) mRNA, complete cds
9768	19064		8.69	1.0E-01	BE537719.1	EST_HUMAN	801065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:341633 5'
9818	19064		8.69	1.0E-01	U23821.1	NT	Saccharomyces cerevisiae suppressor of ABT1 (SAB2) gene, complete cds
9871	19360	28187	1.28	1.0E-01	AJ271046.1	NT	Zen mays mRNA for lcc34-2 protein (lcc348 gene)
9877	19363		4.19	1.0E-01	AF071607.1	NT	Brassica hirsuta genomic DNA, section 1714
						NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pis-R1) mRNA, complete cds
2762	12614	22506	1.09	9.9E-02	AF274008.1	EST_HUMAN	801070210F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3463965 5'
2767	12619	22511	1.44	9.9E-02	BE545564.1	EST_HUMAN	801070210F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3463965 5'
2767	12619	22512	1.44	9.9E-02	BE545564.1	EST_HUMAN	801070210F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3463965 5'
2950	12877	22676	0.62	9.9E-02	AF790747.1	EST_HUMAN	AY790747 H1T Homo sapiens cDNA clone HTFIND05 5'
3228	13153	22952	1.15	9.9E-02	AF069610.1	NT	Homo sapiens neurokin II-alpha gene, partial cds
4652	14472	24280	22.55	9.9E-02	BE674249.1	EST_HUMAN	7d77c12.x1 NCI_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3276968 3'
6191	15118	24662	7.96	9.9E-02	D38710.1	NT	Aspergillus terreus BSD mRNA for blebsidin S deaminase, complete cds
7332	17296	27440	1.5	9.9E-02	6705111	NT	Mus musculus phospholipid transfer protein (Ptp), mRNA
551	10492		1.59	9.9E-02	X63333.1	NT	O salina RAmv3C gene for alpha-amylase
1711	11612	21482	1.53	9.9E-02	4803224	NT	Homo sapiens cyclochrome P-450, subfamily II, polypeptide 1 (CYP2B1) mRNA
3106	13032	22827	3.28	9.9E-02	AF184274.1	NT	Daucus carota esculetinacetylglucosyltransferase 2 (LDOX) mRNA, LDOX-2 allele, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	14031	28605	6.67	9.8E-02	AF297329.1	NT	Leptocaphia maculans beta-tubulin mRNA, complete cds
4131	14031	28606	6.67	9.8E-02	AF297329.1	NT	Leptocaphia maculans beta-tubulin mRNA, complete cds
8755	17604	28148	2.1	9.8E-02	EF037421.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
1328	11295	21092	1.16	9.7E-02	AB004503.1	NT	Alveolar type II cells mRNA for NADP-male enzyme, complete cds
1567	11471		0.98	9.7E-02	4503710	NT	Human alpha-actinin-1 mRNA, complete cds
2214	12100	22004	2.37	9.7E-02	BE169020.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
3901	13511		3.56	9.7E-02	C67065	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5991	13572	29699	1.39	9.7E-02	AF04478.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
6321	16184	28345	4.27	9.7E-02	Z69119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from Z69119 to 3219410
9655	16539	26731	1.59	9.7E-02	N22788.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
9655	16535	26732	1.59	9.7E-02	N22788.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
7137	17014	27207	1.32	9.7E-02	AB53864.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
8531	13403		1.97	9.7E-02	U83337.1	NT	Human alpha-actinin-1 mRNA, complete cds
1889	11802	21785	1.27	9.8E-02	AB00724.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
1939	11802	21794	1.27	9.8E-02	AB00724.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
4248	14147	28621	8.02	9.8E-02	Z52899.2	NT	Proteinase 3-like protein, strain H4320
4932	14870	24979	0.94	9.8E-02	AF066230.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
5083	14893	24798	2.72	9.8E-02	BC061729.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
5713	16921		0.8	9.8E-02	BC010039.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
7602	17371	27580	1.51	9.8E-02	AF067838.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
7677	17527		1.84	9.8E-02	BC064895.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
7712	17622	27845	1.75	9.8E-02	AJ24321.1	NT	Human alpha-actinin-1 mRNA, complete cds
7712	17622	27855	1.75	9.8E-02	AJ24321.1	NT	Human alpha-actinin-1 mRNA, complete cds
7939	17689	27843	1.59	9.8E-02	AB013985.1	NT	Human alpha-actinin-1 mRNA, complete cds
7939	17689	27844	1.59	9.8E-02	AB013985.1	NT	Human alpha-actinin-1 mRNA, complete cds
7989	17796	27860	3.29	9.8E-02	P08174	SWISSPROT	Human alpha-actinin-1 mRNA, complete cds
8125	18013	28260	6.51	9.8E-02	Z76702.1	NT	Human alpha-actinin-1 mRNA, complete cds
8597	18764	28035	1.8	9.8E-02	AA025795.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
9799	19312		1.39	9.8E-02	H14599.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
9849	19344	29212	1.26	9.8E-02	BE738219.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
4012	13918	22564	2.25	9.8E-02	AF196235.1	EST_HUMAN	Human alpha-actinin-1 mRNA, complete cds
5062	14932	24704	0.87	9.8E-02	U93374.1	NT	Human alpha-actinin-1 mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2180	12067		2.2	9.2E-02	R64159.1	EST_HUMAN	y98077.1 Soares infant brain INB Homo sapiens cDNA clone IMAGE:41618 5'
3142	13067	22666	4.83	9.2E-02	C28203.1	SWISSPROT	MAJOR EPIDIDYMUS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3265	13188	22966	1.16	9.2E-02	A4534354.1	EST_HUMAN	n79601.1 NG_OGAP_Cod Homo sapiens cDNA clone IMAGE:528193 3'
3637	13453		1.12	9.2E-02	8755216	NT	Mus musculus p1a-1 call antigen receptor alpha (P1ca), mRNA
4145	14045		1.34	9.2E-02	U62048.1	NT	Human herpesvirus 1 strain KOS-83, latency-associated transcript, promoter region
4211	14109		1.02	9.2E-02	BE296722.1	EST_HUMAN	000944395F1 NH_LMG_17 Homo sapiens cDNA clone IMAGE:260176 5'
4538	14431	24273	1.85	9.2E-02	X06402.1	NT	G gallus M1a-CX gene
6970	16550	26746	1.85	9.2E-02	T46920.1	EST_HUMAN	y98009.1 Stratigene placenta (#637225) Homo sapiens cDNA clone IMAGE:6806 5' similar to
6766	16535	25823	2.07	9.2E-02	X65255.1	NT	gbX59009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
417	6984	18776	2.77	9.1E-02	X77695.1	NT	H. vulgare xylanase isomerase gene
2365	12245	22139	1.01	9.1E-02	X77695	SWISSPROT	O. cuniculus k12 keratin gene
3618	13532		1.14	9.1E-02	AV372969.1	EST_HUMAN	8-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) [PHOSPHOHEXOKINASE]
4383	14278	24058	1.81	9.1E-02	AL161554.2	NT	PAU210349-191259-001-102 BT0349 Homo sapiens cDNA
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5507	15425	25497	1.73	9.1E-02	AF129786.1	NT	Homo sapiens MS485 gene, partial cds; and CLUC1, DOAH, G8b, G8c, G8d, G8e, G8f, BATS, G8h, CSK28, BATA, GA, Apo M, BATS, BATA2, AIE-1, -1C7, LST-1, LTB, TNF, and LTA genes, complete cds
6372	16224	25823	11.89	9.1E-02	AV1180588.1	EST_HUMAN	h174405.91 Schwabach fetal brain 03004 Homo sapiens cDNA clone IMAGE:2281696 5'
7838	17638		1.63	9.1E-02	TU2934.1	EST_HUMAN	FB10F-10 Fetal brain, Stratigene Homo sapiens cDNA clone FB10F0.3 3' end
9021	18816		1.29	9.1E-02	9633464	NT	Bacteriophage M1, complete genome
9269	18692		1.52	9.1E-02	AA176901.1	EST_HUMAN	258b12.21 Stratigene muscle 037209 Homo sapiens cDNA clone IMAGE:617783 3' similar to
9786	19548		5.53	9.1E-02	AJ297380.1	NT	SW17RT13 HUMAN P43070 TROPONIN T1 FAST SKELETAL MUSCLE, ISOFORM BETA 1 ; Homo sapiens partial MUC3B gene for MUC3B much, exons 1-11
							FOLATE RECEPTOR ALPHA PRECURSOR (FRA-ALPHA) [FOLATE RECEPTOR 1] [FOLATE RECEPTOR, ADULT] [ADULT FOLATE-BINDING PROTEIN] (FBP) [OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18] (KB CELLS FBP)
727	10959	20140	3.39	9.0E-02	P15328	SWISSPROT	h10910.1 NG_OGAP_Luc2 Homo sapiens cDNA clone IMAGE:3175942 3' similar to contains Ala repetitive element
1617	11521	21379	6.45	9.0E-02	BC220482.1	EST_HUMAN	repative element
2772	12934	22528	1.11	9.0E-02	AF138522.1	NT	HIV-1 p60gag-05 from USA envelope glycoprotein (env) gene, partial cds
2772	12934	22528	1.11	9.0E-02	AF138522.1	NT	HIV-1 p60gag-05 from USA envelope glycoprotein (env) gene, partial cds
3262	13218	23018	0.82	9.0E-02	AF279193.1	NT	Dicystidellium discoidium spore coat structural protein SP66 (cde), gene, complete cds
4204	14101	23883	0.8	9.0E-02	S68767.1	NT	Concistored-binding globulin (Salmitt salmussusquid monkeys, liver, mRNA, 1474 nt)
4202	14101	23884	0.8	9.0E-02	S68767.1	NT	Concistored-binding globulin (Salmitt salmussusquid monkeys, liver, mRNA, 1474 nt)
4321	14218	24001	1.2	9.0E-02	P65268	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4598	14400	24248	1.79	9.0E-02	X85740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5142	19009	24790	1.06	9.0E-02	C24697	SWISSPROT	REGULATORY PROTEIN ZESTIE
5947	15500	26693	8.02	9.0E-02	W96037.1	EST_HUMAN	z88a42.1 Scores: fetal Jung_NHL19W Homo sapiens cDNA clone IMAGE:267694 5' similar to PIR-S52171 S52171 small G protein - human ;
9607	19428		13.35	9.0E-02		EST_HUMAN	Homo sapiens chromosome 16 open reading frame 5 (C16orf5), mRNA
1419	11325	21159	2.15	8.9E-02	3F701593.1	EST_HUMAN	002125030672 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:428561 5'
1419	11325	21160	2.15	8.9E-02	3F701593.1	EST_HUMAN	002125030672 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:428561 5'
2339	12218	22117	1.41	8.9E-02	3E153721	EST_HUMAN	PNU-H103395-251198-003-401 HT0339 Homo sapiens cDNA
4104	14004		1.71	8.9E-02	4C283055.1	NT	Atchium angustatum AtchP22 protein (AtchP22) gene, partial cds
4534	14427	24208	0.92	8.9E-02	AA424897.1	EST_HUMAN	2003404.1 Scores: NHMMPu_S1 Homo sapiens cDNA clone IMAGE:768169 3'
5599	15485	25559	3.33	8.9E-02	AW483222.1	EST_HUMAN	UH-H83-alc4-09-c1-1 at NCJ_QGAP_Sub8 Homo sapiens cDNA clone IMAGE:3068284 3'
5599	15485	25560	3.33	8.9E-02	AW483222.1	EST_HUMAN	UH-H83-alc4-09-c1-1 at NCJ_QGAP_Sub8 Homo sapiens cDNA clone IMAGE:3068284 3'
5576	15491	25555	3.13	8.9E-02	11433748	NT	Homo sapiens similar to endoglycan (H sapiens) (LOC63107), mRNA
6270	16135	26230	1.55	8.9E-02	947269	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLIDES: METHYLENE TETRAHYDROFOLATE DEHYDROGENASE ; METHYLENE TETRAHYDROFOLATE CYCLOHYDROLASE]
8450	16320		1.83	8.9E-02	770321.1	NT	H sapiens fluorescent chromocoma 6 Hisidil fragment, SC954-2018
8988	16375	27095	5.28	8.9E-02	4C306318.1	EST_HUMAN	EST100187 Liver hepatocellular carcinoma Homo sapiens cDNA, 5' end
9228	18949		4.03	8.9E-02	3F693918.1	EST_HUMAN	002125030672 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:428561 5'
1351	17257	21113	1.25	8.9E-02	C27474	SWISSPROT	PROBABILE DNA LIQASE (POLYDEXYRIBONUCLEOTIDE SYNTHASE [ATP])
3828	13740	25532	0.96	8.9E-02	4C269128.1	EST_HUMAN	EST11568 Uterus Homo sapiens cDNA 5' and
3948	13895		3.24	8.9E-02	000258	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TRID 38 KDa SUBUNIT (TAFL135) (TAFL135) (TAFL135)
4205	14104		1.13	8.9E-02	4690423	NT	Homo sapiens paired box gene 6 (anilidia, xenidia) (PAX6), isoform b, mRNA
7195	17072	27280	1.83	8.9E-02	AA181872.1	EST_HUMAN	z88a40.51 Stradiene octon (8637204) Homo sapiens cDNA clone IMAGE:596288 3'
8461	18334	28958	3.19	8.9E-02	3C204455.1	EST_HUMAN	002125030672 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:393694 5'
8461	18334	28957	3.19	8.9E-02	3C204455.1	EST_HUMAN	002125030672 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:393694 5'
8585	18493	28722	10.63	8.9E-02	ALJ40720.1	EST_HUMAN	DKF2544D1313.1 1434 (synonym: hsc3) Homo sapiens cDNA clone DKF2544D1313 5'
9302	19001	28332	1.38	8.9E-02	Z71661.1	NT	S cerevisiae chromosome XIV reading frame ORF_YNL286w
38356	13540	23337	3.02	8.7E-02	U62095.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xc28S1S protein (XQ28ORF), and glycylcan (GYN) genes, complete cds; and, plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
38356	13540	23337	3.02	8.7E-02	U62095.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xc28S1S protein (XQ28ORF), and glycylcan (GYN) genes, complete cds; and, plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
38356	13540	23337	3.02	8.7E-02	U62095.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xc28S1S protein (XQ28ORF), and glycylcan (GYN) genes, complete cds; and, plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3878	13780	28378	0.62	8.7E-02	U87841.1	EST_HUMAN	2f88402.1 Scores_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA IMAGE:417194 5' similar to contains element MER12 repetitive element
4609	14407	24286	1.22	8.7E-02	AF178536.1	NT	Mus musculus JNK1 interacting protein-3a (Jip3) mRNA, complete cds
5034	14609		1.09	8.7E-02	AE000956.1	NT	Methanobacterium thermoautotrophicum from bases 1175181 to 1189408 (section 101 of 148) of the complete genome
5255	15177	24951	6.41	8.7E-02	AA298375.1	EST_HUMAN	2555508.51 NC1 CGAP GCBT Homo sapiens cDNA clone IMAGE:701438 3'
5255	15177	24952	6.41	8.7E-02	AA298375.1	EST_HUMAN	2555508.51 NC1 CGAP GCBT Homo sapiens cDNA clone IMAGE:701438 3'
8054	17695		2.59	8.7E-02	L04778.1	NT	Oryzopsis cuniculata cytochrome P-450 (CYP4A4) gene, 5' end
8631	18405	28770	1.77	8.7E-02	AJ007763.1	NT	Gluconolactonase cDNAs RNA-1a and RNA-1a genes
9263	18604		2.59	8.7E-02	AJ007763.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
9494	19105		1.81	8.7E-02	X17116.1	NT	Mus musculus nidogen 2 (Nid2) mRNA
1232	11139	20901	7.05	8.0E-02	AJ271758.1	NT	Homo sapiens Xq pseudautosomal region: segment 22
2197	12034	21966	2.22	8.0E-02	BC409597.1	EST_HUMAN	801304016F1 NH1 MGC 21 Homo sapiens cDNA clone IMAGE:363843 5'
3151	13076	22876	2.94	8.0E-02	L05498.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3693	13607		3.07	8.0E-02	AF153393.1	NT	Dipodomys deserti adenylyl cyclase (aca) gene, complete cds
4386	14291	24000	0.87	8.0E-02	J98170.1	NT	Oryzopsis cuniculata glucan-3 gene, untranscribed zone and 5' flanking region
5708	15516	25718	1.39	8.0E-02	Y10326.1	NT	Homo sapiens LCH10 gene
5940	15752	25677	1.51	8.0E-02	J00440.1	NT	Mouse germline 19H chain gene, D region, D-92, mu switch region (part a)
5940	15752	25688	1.51	8.0E-02	J00440.1	NT	Mouse germline 19H chain gene, D region, D-92, mu switch region (part a)
6528	15808	25685	1.26	8.0E-02	5730059	NT	Homo sapiens Src-related Cdk activator protein (SRCAP) mRNA
6528	15808	25685	1.26	8.0E-02	5730059	NT	Homo sapiens Src-related Cdk activator protein (SRCAP) mRNA
8315	18102	28441	1.98	8.0E-02	AF209551.1	NT	Leucetta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8315	18102	28442	1.98	8.0E-02	AF209551.1	NT	Leucetta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8574	18442	28710	3.93	8.0E-02	BC305068.1	EST_HUMAN	001803437F1 NH1 MGC 17 Homo sapiens cDNA clone IMAGE:419216 5'
8574	18442	28711	3.93	8.0E-02	BC305068.1	EST_HUMAN	001803437F1 NH1 MGC 17 Homo sapiens cDNA clone IMAGE:419216 5'
9738	17847	28131	4.71	8.0E-02	A0201073.1	NT	Arctiolepis fulgidus section 34 of 172 of the complete genome
8958	18670	29648	1.73	8.0E-02	AF250660.1	NT	Bacillus stearothermophilus BarF methylase (fim) and BarF restriction endonuclease (FIR) genes, complete cds
2317	12277	22124	2.87	8.0E-02	AE000952.1	NT	Helicobacter pylori 29695 section 130 of 134 of the complete genome
5900	13419		1.8	8.0E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
7503	18570	25665	6.34	8.0E-02	AF233685.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
7503	18570	25665	6.34	8.0E-02	AF233685.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8315	18102	28441	1.98	8.0E-02	AF209551.1	NT	Mus musculus myosin XV (Myo15) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	QRF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7691	17511	27737	3.07	8.9E-02	BC933024.1	EST_HUMAN	RC4-010037-200700-014-005 OT0037 Homo sapiens cDNA
7691	17511	27738	3.07	8.9E-02	BC933024.1	EST_HUMAN	RC4-010037-200700-014-005 OT0037 Homo sapiens cDNA
8498	18369		11.15	8.9E-02	AF165501.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
8512	18364	28649	4.07	8.9E-02	AF001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
9841	19348		1.39	8.9E-02	AI005968.1	NT	Anthriscum majus mRNA for MYB-related transcription factor
9841	19339		3.28	8.9E-02	AA392384.1	EST_HUMAN	EST72758 Ovary II Homo sapiens cDNA 5' end
2832	12728	22351	4.24	8.4E-02	W69330.1	EST_HUMAN	234441.11 Soares, fetal, heart, NHRI19W Homo sapiens cDNA clone IMAGE:343832 5'
5253	15175	24949	7.82	8.4E-02	BC207183.1	EST_HUMAN	80190456P1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:393433 5'
8019	15023	26053	1.71	8.4E-02	AK024458.1	EST_HUMAN	Homo sapiens mRNA for FLJ00350 protein, partial cds
6360	16500	26755	8.11	8.4E-02	BC505074.1	EST_HUMAN	CAB-310750-260000-162-205 BT0750 Homo sapiens cDNA
7031	17781	28020	1.44	8.4E-02	AF735184.1	EST_HUMAN	aa89010.11 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:2035842 3' similar to TR088312
1965	11859	21748	0.86	8.3E-02	583590	NT	bovine hexogenous mitochondrion, complete genome
1965	11859	21749	0.86	8.3E-02	583590	NT	bovine hexogenous mitochondrion, complete genome
3544	13400	23254	8.19	8.3E-02	P73334	SWISSPROT	HYPOPHYSICAL PROTEIN MG309 HOMOLOG PRECURSOR
3557	13431	23271	0.88	8.3E-02	AF439707.1	EST_HUMAN	H82026.x1 Soares, NHRI19P. S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3557	13431	23272	0.88	8.3E-02	AF439707.1	EST_HUMAN	H82026.x1 Soares, NHRI19P. S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3540	13748	23558	2.82	8.3E-02	AF552583.1	NT	Homo sapiens procoagulant-45 gene, exon 1
9833	19533	26728	3.42	8.3E-02	AF185971.1	NT	Rattus norvegicus cytochrome b protein 2 A-form splice variant (Dp2) mRNA, complete cds
8071	16551		1.47	8.3E-02	AA65295.1	EST_HUMAN	op8110.51 NIH_CGAP_K06 Homo sapiens cDNA clone IMAGE:1562779 3'
6529	16708		1.42	8.3E-02	AF487673.1	EST_HUMAN	op8110.51 NIH_CGAP_K06 Homo sapiens cDNA clone IMAGE:1562779 3'
7498	17398	27573	1.44	8.3E-02	AF58303.1	EST_HUMAN	UBUNTU OF SODIUM POTASSIUM ATPASE LIKE ;
7506	17394		1.94	8.3E-02	AF161595.2	EST_HUMAN	Arbidopsis thaliana DNA chromosome 4, contig fragment No. 81
9807	19095		1.55	8.3E-02	BC606438.1	NT	Arbidopsis thaliana DNA chromosome 4, contig fragment No. 81
1357	11283		7.82	8.2E-02	Y08170.2	NT	Galus gallus mRNA for OBAM protein gamma isoform
1480	11385	21248	1.21	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3038	12654		1.78	8.2E-02	AF18206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3733	13845	23015	1.28	8.2E-02	AF14488.2	NT	Arbidopsis thaliana DNA chromosome 4, contig fragment No. 10
3928	13835		1.11	8.2E-02	AF18206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4187	14037	23942	5.38	8.2E-02	AF4890	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	14037	23943	5.38	8.2E-02	AF4890	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	14037	23944	5.36	8.2E-02	AF4890	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5014	14888	24655	2.82	8.2E-02	U7009.1	NT	Mus musculus zinc transporter (Znt-3) gene, complete cds
5271	15193	24658	1.43	8.2E-02	BE367030.1	EST_HUMAN	6014959791 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3824823 5'
6188	15073	26222	3.14	8.2E-02	AF305955.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
7094	16971	27164	3.13	8.2E-02	AW87128.1	EST_HUMAN	PCP210004-031259-011-405 PT0001 Homo sapiens cDNA
7536	17387	27098	5.33	8.2E-02	U04197.1	NT	Bovine necrotic yellow fever virus RNA-2
7528	17479	27099	2.11	8.2E-02	BE254318.1	EST_HUMAN	601116055F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3365690 5'
5314	15005	26336	4.13	8.2E-02	AE02246.2	NT	Chlamydomonas reinhardtii A233, section 73 of the complete genome
9706	19490		1.84	8.2E-02	AF273505.1	NT	Mus musculus epididymal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1479	11384	21247	1.72	8.1E-02	AB017138.1	NT	Pseudomonas putida midstate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcF, mdcG, mdcH, mdcI, and mdcM genes), complete cds
7793	17553		1.65	8.1E-02	U005150.1	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
8789	18604	28994	3.38	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment H621C002
5	12957	19784	3.28	8.0E-02	AW064053.1	EST_HUMAN	ES1566723 IMAGE resequences, MAGE Homo sapiens cDNA
920	10844	20960	1.33	8.0E-02	U69315.1	NT	Millisium carnosum virus subtype 1, complete genome
1671	12701	21440	10.64	8.0E-02	D28535.1	NT	Human gene for dihydropyrimidin dehydrogenase, complete cds (ecm 1-15)
1671	12701	21441	10.64	8.0E-02	D28535.1	NT	Human gene for dihydropyrimidin dehydrogenase, complete cds (ecm 1-15)
1861	11757	21932	3.9	8.0E-02	BE00710.1	EST_HUMAN	SV40-870347.7/1030-001-038 ET0347 Homo sapiens cDNA
2323	12304	22103	1.01	8.0E-02	U98918.1	NT	Synchocystis sp. PCC3803 complete genome, 1727, 2137289-237289
2323	12304	22104	1.01	8.0E-02	U98918.1	NT	Synchocystis sp. PCC3803 complete genome, 1727, 2137289-237289
2421	12238		4.06	8.0E-02	BF246744.1	EST_HUMAN	407855248F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4075819 5'
2790	10591	20553	0.91	8.0E-02	U623446.1	NT	Deposition associated cyclic nucleotide phosphodiesterase gene, complete cds
2870	12787	22891	1.01	8.0E-02	AL145057.1	NT	Thermoplasma acidophilum complete genome, segment 916
3745	13958	23440	0.64	8.0E-02	AW595118.1	EST_HUMAN	ES1578181 MAGE resequences, MAGE Homo sapiens cDNA
3980	13887		1.06	8.0E-02	4600304	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB2) mRNA
4709	14559		5.62	8.0E-02	U72704.1	NT	Mimivirus gene for guanine B
4834	14710	24498	0.97	8.0E-02	M28071.1	NT	Herpesvirus saimiri transformation-associated protein (STP), and dihydropyrimidine dehydrogenase (DHFR) genes, complete cds, and small nuclear RNAs (snRNAs)
5591	15503	25981	3.35	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6301	15503	25981	1.63	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
6727	16037	26789	3.55	8.0E-02	AL114893.1	NT	Bovine alpha-actinin 4 cDNA library under conditions of nitrogen deprivation
7101	17298	27471	1.46	8.0E-02	X74208.1	NT	H sapiens AGT gene, intron 4
7401	17298	27472	1.46	8.0E-02	X74208.1	NT	H sapiens AGT gene, intron 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Exon Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8172	18060	28310	7.42	8.0E-02	AF17896.1	NT	Homo sapiens SCG10 like protein, helicase-like protein NHL, MBB, and ADP-ribosylation factor related protein 1 (ARFRP-1) genes, complete cds
8344	19023	28500	2.94	8.0E-02	AJ005376.1	NT	Drosophila areva hunchback region
9591	13867		1.47	8.0E-02	4503004	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB1.2) mRNA
9599	19054		3.04	8.0E-02	AJ278495.1	NT	Homo sapiens Ranbp7 gene, Sra1 gene and Wsot gene
2127	12015	21613	3.98	7.9E-02	BE290008.1	EST_HUMAN	U00043191F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2695610 5'
2548	12875	22973	6.43	7.9E-02	AI592029.1	EST_HUMAN	af96003.x1 Barstead colon HPLR87 Homo sapiens cDNA clone IMAGE:273940 3' similar to gb:226876
3776	13688	28471	3.31	7.9E-02	6891044	EST	IOS RIBOSOMAL PROTEIN L38 (HUMAN);
3776	13688	28471	3.31	7.9E-02	6891044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4595	14453	24256	1.09	7.9E-02	BF348454.1	EST_HUMAN	602019770F1 NCI_CGAP_Bln87 Homo sapiens cDNA clone IMAGE:4185401 5'
4705	14602		1.16	7.9E-02	AB00619.1	NT	Scapharhynchus thompsoni RXV24L mRNA, partial cds
6882	16022	28766	3.25	7.9E-02	U27832.1	NT	Scapharhynchus coelacanth suppressor of WIF2 (Smt4g) (SMT4) gene, complete cds
7702	17612	27838	5.98	7.9E-02	A001644.1	EST_HUMAN	cc63005.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WPC-C3742.2
7702	17612	27838	5.98	7.9E-02	A001644.1	EST_HUMAN	cc63005.s1 NCI_CGAP_B2 Homo sapiens cDNA clone IMAGE:1632466 3' similar to WPC-C3742.2
1192	11102	20647	1.43	7.8E-02	AI793275.1	EST_HUMAN	cc63002.y6 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.B.1
1192	11102	20648	1.43	7.8E-02	AI793275.1	EST_HUMAN	cc63002.y6 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.B.1
4688	14674	24371	0.91	7.8E-02	AF386837.1	EST_HUMAN	PHG-FN0005-14700-005-05 FN0005 Homo sapiens cDNA
8019	13603		2.71	7.8E-02	BE290048.1	EST_HUMAN	cc6300505F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2695693 5'
5197	15090	24825	1.04	7.8E-02	A4185020.1	EST_HUMAN	igf2g12.x1 Sources_NIH_T_GSC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10.13 MER10 repetitive element;
7296	17113	27306	2.06	7.8E-02	AF23437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSF1b mRNA, complete cds
7296	17113	27307	2.06	7.8E-02	AF23437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSF1b mRNA, complete cds
7369	17907	27813	1.27	7.8E-02	AA06054.1	EST_HUMAN	nc83006.L1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:771731
1378	12683	21136	1	7.7E-02	AF181697.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3338	13454		2.09	7.7E-02	AJ280003.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
6615	16495	26682	4.4	7.7E-02	AA02848.1	EST_HUMAN	zid3311.1 Sources overy tumor NIH07 Homo sapiens cDNA clone IMAGE:741717 5' similar to TRG1173905 G1173905 associated protein; ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7690	17610	27736	4.62	7.7E-02	P30800	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR069C
8376	18263	28804	5.24	7.7E-02	11422757	NT	Homo sapiens KIA0629 gene product (KIA0629), mRNA
9535	19551		2	7.7E-02	11438658	NT	Homo sapiens Interferon regulatory factor 7 (IRF7), mRNA
3341	13261	23067	2.57	7.6E-02	BE514482.1	EST_HUMAN	60131630F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834603 5'
3362	13261	23067	0.94	7.6E-02	AA29647.1	EST_HUMAN	EST112212 Cerebellar II Homo sapiens cDNA 5' end similar to probactein 43
3512	13428	23220	0.03	7.6E-02	AJ40877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
4765	14650		0.56	7.6E-02	AF155844.1	EST_HUMAN	RC3-CT0347:10300-014-405 CT0347 Homo sapiens cDNA
7393	17311	27518	1.34	7.6E-02	AJ131016.1	NT	Homo sapiens SCL gene locus
7595	17545		1.34	7.6E-02	AL139076.2	NT	Campylobacter jejuni NC10C11168 complete genome, segment 5/9
8627	18736	29028	2.46	7.6E-02	AF109546.1	EST_HUMAN	QV3-8N00048-160405-161-e04 EN00048 Homo sapiens cDNA
767	10698	20535	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	10698	20535	1.13	7.5E-02	5902093	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1878	11774	21646	0.97	7.5E-02	AL163278.2	NT	Homo sapiens chromosome 21, segment H821C078
4407	14501	24086	0.84	7.5E-02	AB015861.1	NT	Homo sapiens IL18 gene for Interleukin-18, intron 1 and exon 2
6855	16734	26527	1.19	7.5E-02	AB84397.1	EST_HUMAN	W63002x1 NCL_GCAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:1744329 ALPHA
9853	16831	27024	1.21	7.5E-02	AF116913.1	EST_HUMAN	ENKASE (HUMAN)
4498	10123	20231	1.23	7.4E-02	AF1633547.1	EST_HUMAN	AL116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
1444	11349		1.08	7.4E-02	AF530271.1	NT	Equus caballus 1 salmon NS30597, complete genome
2358	12410		0.93	7.4E-02	675069	NT	Mus musculus parvalbumin nontranscribed transcription factor 1 (Pval1), mRNA
3545	13451	23265	0.88	7.4E-02	AB07865.1	EST_HUMAN	WHS301X1 Scavenger, NLR1_GPC_S1 Homo sapiens cDNA clone IMAGE:238585 5'
4860	14464	24262	3.38	7.4E-02	AF530271.1	NT	Homo sapiens ADP-ATP carrier protein (ANT1-2) gene, complete cds
4897	14738	24518	2.06	7.4E-02	6978442	NT	Rattus norvegicus Actin receptor like kinase 1 (Rorrl), mRNA
4898	14738	24518	1.7	7.4E-02	6978442	NT	Rattus norvegicus Actin receptor like kinase 1 (Rorrl), mRNA
5913	15919		1.75	7.4E-02	671477.1	EST_HUMAN	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Ubrp), mRNA
6012	16482	26678	1.4	7.4E-02	SE88012.1	EST_HUMAN	Yg1465011 Soares infant brain NIH Homo sapiens cDNA clone IMAGE:352339 5'
6950	16628	27021	1.37	7.4E-02	U90939.1	NT	60146330F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:386524 5'
9271	18675		2.08	7.4E-02	1152860	NT	Human perlecan tropoelastin protein 2 (PWP2) gene, exons 15 to 21, complete cds
9527	18674		2.82	7.4E-02	AF376943.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (HDAC5), mRNA
9678	19235	25242	1.81	7.4E-02	AF505069.1	EST_HUMAN	CHM4H10293-081199-037-411 HT0243 Homo sapiens cDNA
461	10405	20222	0.95	7.3E-02	BE964961.2	EST_HUMAN	001463313F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3867738 5'
							001698738F1 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:3865209 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
461	10105	20223	0.66	7.3E-02	BE04061.2	EST_HUMAN	0616957387 NH1_MGC_39 Homo sapiens cDNA clone IMAGE:389206 3'
669	10003	20420	2.73	7.3E-02	AE00789.1	NT	Thermodesulfobacterium section 101 of 189 of the complete genome
1465	12965	21237	3.04	7.3E-02	AW000281.1	EST_HUMAN	OMC-NT1004-130300-284-g08 NT1004 Homo sapiens cDNA
1801	12705	21237	14.81	7.3E-02	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4827	14906		1.01	7.3E-02	U11283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
8413	16275	20437	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8413	16275	26438	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6749	16029		1.27	7.3E-02	7662107	NT	Homo sapiens KIA03424 protein (KIA03424), mRNA
8548	15789	25910	2.78	7.3E-02	AA176977.1	EST_HUMAN	424042.x1 Sorex, fetal liver, spleen, INFLS.31 Homo sapiens cDNA clone IMAGE:481778 3' similar to gbl-L04235 26S PROTEASE SUBUNIT 4 (HUMAN);
114	10093	19811	0.94	7.2E-02	AE000832.1	NT	Methanobacterium thermoautotrophicum from basins 1029155 to 1036524 (section 68 of 148) of the complete genome
114	10093	19812	0.94	7.2E-02	AE000832.1	NT	Methanobacterium thermoautotrophicum from basins 1029155 to 1036524 (section 68 of 148) of the complete genome
1480	11065	21228	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1480	11065	21229	2.23	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2502	12372		2.5	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3810	13771	23511	0.82	7.2E-02	AW296323.1	EST_HUMAN	U1-HW10-28-04-01.11 NC1 CGAP_S168 Homo sapiens cDNA clone IMAGE:279206 3'
4248	14146	23622	4.02	7.2E-02	E5F52307.1	EST_HUMAN	60307751F1 NH1_MGC_02 Homo sapiens cDNA clone IMAGE:425196 5'
4594	14423	24268	78.82	7.2E-02	U1469583	NT	Rhodospirillum rubrum salivary mitochondrion, complete genome
4597	14472	24268	0.94	7.2E-02	AB011921.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5230	15154	24823	3.03	7.2E-02	U07531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5231	15155	24823	7.62	7.2E-02	U11120	SWISSPROT	CALMODULIN
6252	16118	26272	9.33	7.2E-02	BF210066.1	EST_HUMAN	STRONGID358F1 NH1_MGC_37 Homo sapiens cDNA clone IMAGE:4065710 5'
6281	16145		1.76	7.2E-02	5831897	NT	Strongyloides purpuratus mitochondrion, complete genome
7545	17366	27008	2.05	7.2E-02	AY12432.1	EST_HUMAN	AY172482 DCA Homo sapiens cDNA clone DCAUG01 5'
7625	17476	27097	4.23	7.2E-02	U14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splicing product, partial cds
7746	17696	27918	2.84	7.2E-02	AW673187.1	EST_HUMAN	hq2411.x1 NC1_OGAP_A41 Homo sapiens cDNA clone IMAGE:3120833 3' similar to TRQ82540 Q02340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
7820	17776	28016	2.05	7.2E-02	U62995.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed Xq28TS protein (XQ28ORF), and biglycan (BSN) gene, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7693	17633	28073	5.47	7.2E-02	BE560003.1	EST_HUMAN	60134926F1 NIH_MGC_58 Homo sapiens cDNA, clone IMAGE:3685651 5'
7694	17644		3.2	7.2E-02	BE558214.1	EST_HUMAN	60100504F1 NIH_MGC_10 Homo sapiens cDNA, clone IMAGE:3451559 5'
8285	18164	28407	4.8	7.2E-02	AF076674.1	NT	Reltux nervegrowth factor DLH1 transcription factor Maf1 (Maf1) gene, complete cds
9178	18019	25346	1.44	7.2E-02	AAT73595.1	EST_HUMAN	AF160411 Soares, NIH/NIH, S1 Homo sapiens cDNA, clone IMAGE:1048398 5'
9214	18042		3.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seraniki P) Homo sapiens cDNA, clone PS18D2 3'
9273	18077		1.44	7.2E-02	A4594455.1	EST_HUMAN	nc05906.s1 NCL_O3AP_Phet Homo sapiens cDNA, clone IMAGE:1069839 3'
9332	18013		1.62	7.2E-02	U63828.1	NT	Homo sapiens alpha 1-microglobulin (A1M) gene, complete cds
9346	18031		3.80	7.2E-02	AW900982.1	EST_HUMAN	GM44NN1009-200302-118-111 NN1009 Homo sapiens cDNA
1832	11759	21633	1.55	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (Dp) proviral structural capsid protein (gag) gene, partial cds
2243	12127		0.9	7.1E-02	AE004800.1	EST_HUMAN	Pseudomonas aeruginosa PAO1, section 461 of 529 of the complete genome
2247	12131	22028	5.09	7.1E-02	EF238602.1	EST_HUMAN	60187226F1 NIH_MGC_58 Homo sapiens cDNA, clone IMAGE:4052881 5'
9603	18044		1.93	7.1E-02	BE330754.1	EST_HUMAN	60114387F1 NIH_MGC_14 Homo sapiens cDNA, clone IMAGE:3061234 5'
517	10438	20270	1.23	7.0E-02	Q07962	SWISSPROT	COLLAGEN ALPHA (XV) CHAIN PRECURSOR
1464	11399		1.46	7.0E-02	X63677.1	NT	M. trinitatis MtrcA-1 gene
1725	11628	21465	1.35	7.0E-02	A036343.1	EST_HUMAN	258004.s1 Stratagene cDNA (2587234) Homo sapiens cDNA, clone IMAGE:505559 3'
2694	12622	27215	1.72	7.0E-02	AW139152.1	EST_HUMAN	UHF8B1-acy-co-7-QJ161 NCT_O3AP_S063 Homo sapiens cDNA, clone IMAGE:2716020 3'
3928	13734	25523	1	7.0E-02	AA816488.1	EST_HUMAN	af012.s1 Soares, testis NCT_Homo sapiens cDNA, clone 1375676 3' similar to gbX03002.063
3932	13866	23642	1.24	7.0E-02	BE070294.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN)
4047	13946		1.08	7.0E-02	AW762952.1	EST_HUMAN	QV4310407-280100-050-510 BT0407 Homo sapiens cDNA
4121	14021	23769	1.27	7.0E-02	AF077821.1	NT	CmG-UM0001-060306-270-612 UM0071 Homo sapiens cDNA
4846	14727	24510	7.1	7.0E-02	EF381987.1	EST_HUMAN	CmG family inducible nitric oxide synthase mRNA, complete cds
7256	17136	27329	1.25	7.0E-02	9528113	EST_HUMAN	60187262F1 NIH_MGC_58 Homo sapiens cDNA, clone IMAGE:4050071 5'
7634	17395	27597	1.19	7.0E-02	K02801.1	NT	African swine fever virus, complete genome
3371	13127		1.31	6.9E-02	4507968	NT	Rat Ig gamma 1 epsilon H-chain gene C-region, 3' end
3714	13636	23421	1.42	6.9E-02	Q06364	SWISSPROT	af09405.s1 Soares, NCT_GBC_S1 Homo sapiens cDNA, clone IMAGE:1327184 3' similar to gb1.14837
8070	18667	28950	2.39	7.0E-02	AA74295.1	EST_HUMAN	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
503	10445	20256	5.34	6.9E-02	AF163210.2	NT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
503	10445	20257	5.34	6.9E-02	AF163210.2	NT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5100	14698		1.05	6.9E-02	AF079906.1	NT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6978	18655	27048	1.37	6.9E-02	BE607435.1	EST_HUMAN	80134066.F1 NF1_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
6978	18655	27049	1.37	6.9E-02	BE607435.1	EST_HUMAN	80134066.F1 NF1_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9208	18639		3.95	6.9E-02	X74315.1	NT	X.lavris VF02 mRNA for fork head protein
9395	19045		1.5	6.9E-02	P44921	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFQ HOMOLOG
9598	19160		2.19	6.9E-02	AF165963.1	NT	Homo sapiens membrane-bound antipeptidase P (NPEP2) gene, complete cds
1839	11736	21610	1.11	6.9E-02	AA46759.1	EST_HUMAN	ac0002.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:497339 5' similar to gb:M22382
1839	11736	21611	1.11	6.9E-02	AA46759.1	EST_HUMAN	ac0002.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:497339 5' similar to gb:M22382
1895	11761	21635	3.91	6.9E-02	AF169373.1	EST_HUMAN	MITOCHONDRIAL MATRIX PROTEIN P1: PRECURSOR (HUMAN);
3032	12899	22780	1.23	6.9E-02	AJ276296.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSOR1) gene, complete cds
3032	12899	22781	1.23	6.9E-02	AJ276296.1	EST_HUMAN	af15605.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376528 3'
3032	12899	22782	1.23	6.9E-02	AJ276296.1	EST_HUMAN	af15605.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376528 3'
4463	14347		0.92	6.9E-02	BC141076.1	EST_HUMAN	af15605.s1 Soares_testis_NHT Homo sapiens cDNA clone 1376528 3'
6315	16178	26337	7.71	6.9E-02	AJ163288.2	NT	Oncohyndus mykiss TAP1 protein (OnmyTAP1) mRNA, complete cds
6822	16701	26864	6.12	6.9E-02	AJ26287.1	EST_HUMAN	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841403 3'
6822	16701	26865	1.37	6.9E-02	T03214.1	EST_HUMAN	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841403 3'
9011	16719		2.67	6.9E-02	AA78014.1	EST_HUMAN	Homo sapiens chromosome 21 segment H521 C088
9140	16865		2.67	6.9E-02	AA78014.1	EST_HUMAN	Pyrococcus abyssi complete genome, segment 516
9764	19294		2.67	6.9E-02	6910595	NT	Pyrococcus abyssi complete genome, segment 516
1511	11416	21622	2.17	6.7E-02	AF115938.1	NT	FB448 Fetal brain, Stratiotes Homo sapiens cDNA clone FB448 3' end similar to LINE-1
1851	11474		2.5	6.7E-02	AJ29285.1	EST_HUMAN	af15605.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320709 3'
3656	13570	23356	3.52	6.7E-02	P17279	SWISSPROT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1326	11233	21089	1.05	6.9E-02	AF136509.1	EST_HUMAN	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
1347	11253	21103	1.5	6.9E-02	AF245118.1	NT	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
3133	12021	21918	3.07	6.9E-02	AJ289241.1	NT	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
3133	13058		1.32	6.9E-02	Q13585	SWISSPROT	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
3418	13335	23136	8.91	6.9E-02	R64305.1	EST_HUMAN	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
3432	13349	23164	2.19	6.9E-02	7108357	NT	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
3432	13349	23165	2.19	6.9E-02	7108357	NT	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
3989	13995	29873	1.56	6.9E-02	AF290225.1	NT	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
4904	14764	24658	8.4	6.9E-02	Q61703	SWISSPROT	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to
4904	14764	24659	8.4	6.9E-02	Q61703	SWISSPROT	af15605.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2384020 3' similar to

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	OPF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5167	15033	24800	1.34	6.8E-02	AF204882.1	NT	Ameaeta albipennis nucleopolydnavirus AcO3BF-17 hemidog gene, complete cds
5190	15033	24817	0.84	6.8E-02	AF004346.1	NT	Vibrio cholerae chromosome II, section 2 of 88 of the complete chromosome
5938	15093	25688	3.09	6.8E-02	X09411.1	NT	P. vulgaris mRNA for chalcone synthase
6209	15099	29105	2.93	6.8E-02	AI243263.1	EST HUMAN	gh141001.x1 Source, NFI, T, GBC, S1 Homo sapiens cDNA clone IMAGE:1847293.3
6635	15615	29706	1.49	6.8E-02	AF002572.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
7608	17656	27694	1.37	6.8E-02	Y07848.1	NT	Homo sapiens EWS, gwi22, np22, np22 and bcr/abl genes
8330	18207	28457	0.28	6.8E-02	BF374248.1	EST HUMAN	MR1-SN0064-01090-003-412 SN0064 Homo sapiens cDNA
9533	19175		2.08	6.8E-02	9937694.1	NT	Mus musculus DIP8 gene (Dip8), mRNA
9832	19395		1.46	6.8E-02	AF167430.1	NT	Rattus norvegicus cytochrome P450, ZET (CYP2E1) gene, 5' flanking region
6971	10506	20313	1.91	6.8E-02	BF027693.1	EST HUMAN	901671046F1.NH1.MGC_20 Homo sapiens cDNA clone IMAGE:3954178.5
6771	10595	20749	1.78	6.8E-02	7708068	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1359	12755	21131	4.17	6.8E-02	U17624.1	NT	Xenopus laevis alpha(E) casein mRNA, complete cds
1702	17603	21474	2.16	6.8E-02	AE000784.1	NT	Aquifex solifarius section 98 of 109 of the complete genome
5413	15333	25393	1.76	6.8E-02	AA140991.1	EST HUMAN	ph6812.x1 Source, cory, human, NH207 Homo sapiens cDNA clone IMAGE:765743.3 similar to gb-M26038
8035	17927	28173	6.61	6.8E-02	AF163948.1	EST HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-B BETA, CHAIN (HLA-DRB1)
8334	18623		3.53	6.8E-02	M21495.1	NT	Redbet microsatellite repeats hypodermis
9383	18051		3.73	6.8E-02	AF102893.1	NT	Nectia haematodes linear related protein 2 (LRF2) gene, complete cds
691	10501	20307	1.63	6.8E-02	X61549.1	NT	A. canisare precursor of purkinje-cellular protein (PCP) gene
4802	12609	22708	1.35	6.8E-02	6999523	NT	Mus musculus histone desoxyase 5 (Hds5), mRNA
5190	15044		8.78	6.8E-02	6999523	NT	Mus musculus histone desoxyase 5 (Hds5), mRNA
6349	15297	25064	1.4	6.8E-02	AI191696.1	EST HUMAN	qp07041.x1 Source, testis, NHT Homo sapiens cDNA clone IMAGE:1739249.3 similar to contains LTRB.53
5718	15525	25727	7.58	6.8E-02	AF052733.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofel gene, and sodium phosphate transporters (NPT3) gene, complete cds
5718	15525	25728	7.58	6.8E-02	AF052733.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofel gene, and sodium phosphate transporters (NPT3) gene, complete cds
9079	15092	29210	5.23	6.8E-02	BE974448.1	EST HUMAN	601680429R2.NH1.MGC_33 Homo sapiens cDNA clone IMAGE:3960503.3
9853	18732		2.57	6.8E-02	6753323	NT	Mus musculus chaperonin subunit 6a (cna), mRNA
7034	18911	27099	4.12	6.8E-02	AA063905.1	EST HUMAN	h1419.aeq.2 Human fetal heart, Lambda ZAP Express-Homo sapiens cDNA.3'
7603	17454	27683	2.02	6.8E-02	AB011126.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
8946	18754	29049	1.85	6.8E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofel gene, and sodium phosphate transporters (NPT3) gene, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (BLAST E Value)	Top Hit Association No.	Top Hit Database Source	Top Hit Descriptor
8646	18754	29250	1.86	6.4E-02/U91825.1	NT	NT	Human hereditary haemochromatosis (HLA-H) gene, RefSeq, and sodium phosphatase transporter (NPT3) gene, complete cds
9299	19035		3.65	6.4E-02/AF107590.1	NT	NT	Homo sapiens multi-95 (MUC95) gene, partial cds
9337	19017	20295	2.27	6.4E-02/AJ27174.1	NT	NT	Drosophila melanogaster mRNA for mod(mdg)/91.4 protein
1720	11921	21490	2.43	6.3E-02/AF105905.1	NT	NT	Mus musculus major histocompatibility locus class III regions Hc2701 gene, partial cds; eMRNP, G7A, NG23, MuS homolog, QLC2, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3552	13467		2.05	6.3E-02/P37092	SWISSPROT		HEAT SHOCK PROTEIN 70 HOMOLOG
7752	17602	27235	3.14	6.3E-02/AB010162.1	NT	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CNR-162
8098	16837	25741	3.28	6.3E-02/BF127360.1	EST_HUMAN		601873316F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE409709.6
9373	18039		1.46	6.3E-02/P19276	SWISSPROT		TRANSORPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3)
4157	14057	23831	3.37	6.2E-02/AL161872.2	NT	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4343	14142		1.11	6.2E-02/AF271738.1	NT	NT	Rolla nonreplicative differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4379	14373		6.41	6.2E-02/C62109.1	SWISSPROT		52 KD RO PROTEIN (SLOGREN'S DROMORE TYPE A ANTIGEN (SS-A)) (RCSS-A)) (RC82)
4933	14887		1.22	6.2E-02/AY068701.1	EST_HUMAN		AY705191 AQB Homo sapiens cDNA clone ADB8A503.6
7450	17310	27235	1.21	6.2E-02	8977893	NT	Mus musculus stromal cell derived factor receptor 2 (Sdr2), mRNA
8650	18344	28327	1.84	6.2E-02/AJ242735.1	NT	NT	Measurium antisense mRNA for chondrocyte 391 gene
9720	19722		3.50	6.2E-02/AE00750.1	NT	NT	Aquatic animal vector 83 of 103 of the complete genome
9841	19142	25266	1.98	6.2E-02/BF112939.1	EST_HUMAN		757068.01 Source_XBT_Fg_391_OT_P31 Homo sapiens cDNA clone IMAGE392381.5 similar to TR001450 HSP40 HSP70 HSP90 HSP100 HSP125 HSP170 HSP27 HSP30 HSP36 HSP39 HSP40 HSP42 HSP47 HSP49 HSP50 HSP54 HSP56 HSP58 HSP59 HSP60 HSP62 HSP63 HSP64 HSP65 HSP66 HSP67 HSP68 HSP69 HSP70 HSP71 HSP72 HSP73 HSP74 HSP75 HSP76 HSP77 HSP78 HSP79 HSP80 HSP81 HSP82 HSP83 HSP84 HSP85 HSP86 HSP87 HSP88 HSP89 HSP90 HSP91 HSP92 HSP93 HSP94 HSP95 HSP96 HSP97 HSP98 HSP99 HSP100 HSP101 HSP102 HSP103 HSP104 HSP105 HSP106 HSP107 HSP108 HSP109 HSP110 HSP111 HSP112 HSP113 HSP114 HSP115 HSP116 HSP117 HSP118 HSP119 HSP120 HSP121 HSP122 HSP123 HSP124 HSP125 HSP126 HSP127 HSP128 HSP129 HSP130 HSP131 HSP132 HSP133 HSP134 HSP135 HSP136 HSP137 HSP138 HSP139 HSP140 HSP141 HSP142 HSP143 HSP144 HSP145 HSP146 HSP147 HSP148 HSP149 HSP150 HSP151 HSP152 HSP153 HSP154 HSP155 HSP156 HSP157 HSP158 HSP159 HSP160 HSP161 HSP162 HSP163 HSP164 HSP165 HSP166 HSP167 HSP168 HSP169 HSP170 HSP171 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HSP887 HSP888 HSP889 HSP890 HSP891 HSP892 HSP893 HSP894 HSP895 HSP896 HSP897 HSP898 HSP899 HSP900 HSP901 HSP902 HSP903 HSP904 HSP905 HSP906 HSP907 HSP908 HSP909 HSP910 HSP911 HSP912 HSP913 HSP914 HSP915 HSP916 HSP917 HSP918 HSP919 HSP920 HSP921 HSP922 HSP923 HSP924 HSP925 HSP926 HSP927 HSP928 HSP929 HSP930 HSP931 HSP932 HSP933 HSP934 HSP935 HSP936 HSP937 HSP938 HSP939 HSP940 HSP941 HSP942 HSP943 HSP944 HSP945 HSP946 HSP947 HSP948 HSP949 HSP950 HSP951 HSP952 HSP953 HSP954 HSP955 HSP956 HSP957 HSP958 HSP959 HSP960 HSP961 HSP962 HSP963 HSP964 HSP965 HSP966 HSP967 HSP968 HSP969 HSP970 HSP971 HSP972 HSP973 HSP974 HSP975 HSP976 HSP977 HSP978 HSP979 HSP980 HSP981 HSP982 HSP983 HSP984 HSP985 HSP986 HSP987 HSP988 HSP989 HSP990 HSP991 HSP992 HSP993 HSP994 HSP995 HSP996 HSP997 HSP998 HSP999 HSP1000 HSP1001 HSP1002 HSP1003 HSP1004 HSP1005 HSP1006 HSP1007 HSP1008 HSP1009 HSP1010 HSP1011 HSP1012 HSP1013 HSP1014 HSP1015 HSP1016 HSP1017 HSP1018 HSP1019 HSP1020 HSP1021 HSP1022 HSP1023 HSP1024 HSP1025 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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
29005	10076	18963	1.22	6.0E-02	AA168730.1	EST_HUMAN	ap7604.1 Stragiplegi HeLa cell 53 837216 Homo sapiens cDNA clone IMAGE:026310 5'
3101	13116	23921	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Odon didemacronatae IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3191	13116	23922	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Odon didemacronatae IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3583	13497	24551	0.9	6.0E-02	BE964443.2	EST_HUMAN	EST155815091 NH ₂ MGC_59 Homo sapiens cDNA clone IMAGE:3876060 3'
4893	14773	24551	1.17	6.0E-02	2617739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5814	15235	24551	3.49	6.0E-02	AW370211.1	EST_HUMAN	Homo sapiens stimulated trans-acting factor (50 kb) (STAF50) mRNA
6172	16129	24848	2.89	6.0E-02	5174988	NT	Homo sapiens stimulated trans-acting factor (50 kb) (STAF50) mRNA
6172	16129	24848	2.89	6.0E-02	5174988	NT	Homo sapiens stimulated trans-acting factor (50 kb) (STAF50) mRNA
6255	16130	26284	1.67	6.0E-02	BF38249.1	EST_HUMAN	6018162472 NH ₂ MGC_59 Homo sapiens cDNA clone IMAGE:4049220 5'
6524	16383	26552	2.05	6.0E-02	AI04276.1	EST_HUMAN	658008.x1 Scores: 1656 NHT Homo sapiens cDNA clone IMAGE:1754109 3'
7340	17208	27409	1.19	6.0E-02	AI023167.1	EST_HUMAN	175406.x1 NCL_OGAP_608 Homo sapiens cDNA clone IMAGE:2237392 3'
7340	17208	27409	1.19	6.0E-02	AI023167.1	EST_HUMAN	175406.x1 NCL_OGAP_608 Homo sapiens cDNA clone IMAGE:2237392 3'
7411	17278	27465	1.79	6.0E-02	AJ243555.1	NT	Adiponectin (Adipon) gene for immunoglobulin light chain variable region, exon 1-2
7411	17278	27467	1.79	6.0E-02	AJ243555.1	NT	Adiponectin (Adipon) gene for immunoglobulin light chain variable region, exon 1-2
8538	18016	28254	1.95	6.0E-02	1145172	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2) mRNA
9715	18288		1.84	6.0E-02	AI06273.1	EST_HUMAN	w68003.x1 Scores: 11571 GBC_51 Homo sapiens cDNA clone IMAGE:2303085 3' similar to TR-060258
229	10198	20011	3.42	5.9E-02	AW55479.1	EST_HUMAN	002388 KIAA0051 PROTON
2905	12852	22681	2.59	5.9E-02	AF160289.1	NT	RC-101000F-260100-072410 DT0001 Homo sapiens cDNA
4770	14655	24443	0.89	5.9E-02	AF006394.1	NT	Yus muscularis p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
7008	18895	27077	1.87	5.9E-02	0055249	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP) gene, complete cds
5165	18043		2.72	5.9E-02	0079970	NT	Mus musculus troponin, isolated homodimer 5 (Troponin5) (Tn5), mRNA
8383	18290	28519	3.15	5.9E-02	11453356	NT	Mus musculus follistatin-like (Foll), mRNA
8842	18655		1.99	5.9E-02	AJ240733.1	NT	Homo sapiens thinin (LOC51199), mRNA
917	10841		4.35	5.9E-02	D00110.1	NT	Cellular gallus HCCs telomere junction
2830	12769	23314	1.1	5.9E-02	AJ229621.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
3813	13527	23314	1.44	5.9E-02	AE001175.1	NT	Populus trichocarpa COX2/COX1 gene, exon 1 to exon 5
4257	14166	23831	4.39	5.9E-02	AW051927.1	EST_HUMAN	Thermobacillus maritima section 87 of 136 of the complete genome
4257	14166	23832	4.36	5.9E-02	AW051927.1	EST_HUMAN	w02402.x1 NCL_OGAP_K6411 Homo sapiens cDNA clone IMAGE:2544578 3'
4447	14341	24132	4.21	5.9E-02	AI047505.1	EST_HUMAN	w02402.x1 NCL_OGAP_K6411 Homo sapiens cDNA clone IMAGE:2544578 3'
4447	14341	24133	4.21	5.9E-02	AI047505.1	EST_HUMAN	q5M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN)
4471	14355		2.04	5.9E-02	AF090244.1	NT	q5M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN)
4471	14355		2.04	5.9E-02	AF090244.1	NT	q5M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); Gallus gallus tyrosine kinase-JAK1 (JAK1) mRNA, complete cds

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6523	13332	29560	2.78	5.9E-02	M99150.1	NT	Human polymorphic microsatellite DNA
6523	13332	29561	2.76	6.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
9227	19548		2.34	5.8E-02	AF22077.1	NT	Drosophila melanogaster male fulltest type-A (fru) mRNA, complete cds
6518	19735		4.56	5.8E-02	AA604259.1	EST_HUMAN	no75611.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:112884.3
3018	12946	22738	1.34	5.7E-02	AB81644.1	EST_HUMAN	cd3303.s1 NCL CGAP_B2 Homo sapiens cDNA clone IMAGE:1632465.3 similar to WP_C57A2.2
3033	12941	22764	1.34	5.7E-02	AB81644.1	EST_HUMAN	Human serpin dopamine transporter (SLC6A3) gene, complete cds
9731	13643	29428	1.8	5.7E-02	AF168079.1	EST_HUMAN	EST176965 IMAGE resequences, MAGI Homo sapiens cDNA
6740	16619	23608	1.42	5.7E-02	AL266390.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv2.2 gene)
8524	18306	28961	3.80	5.7E-02	AF152955.1	EST_HUMAN	cn18609.v1 Normal Human Tibrocular Bone Cells Homo sapiens cDNA clone NHTBC_cn18609 random
8524	18306	28962	3.86	5.7E-02	AF152955.1	EST_HUMAN	cn18609.v1 Normal Human Tibrocular Bone Cells Homo sapiens cDNA clone NHTBC_cn18609 random
9437	16558		5.55	5.7E-02	AF03200.1	NT	Phi DNA for SPAL2, complete cds
9532	18530		2.97	5.7E-02	AF217400.1	NT	Homo sapiens fragile 160 acid reductase (FOR) gene, exon 8, 9, and partial cds
9798	19727		3.82	5.7E-02	AF261265.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
1510	11415	21274	0.86	5.6E-02	AF064455.1	NT	Hydroxycysteine reductase ribosomal protein L18 (p115) gene, intron; chloroplast gene for chloroplast product
4540	14433	24215	1.26	5.6E-02	AB019100.1	NT	Lycopodium obscurum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4598	14460	24272	1.14	5.6E-02	AA320593.1	EST_HUMAN	zef5cd.s1 NCL CGAP_L2 Homo sapiens cDNA clone IMAGE:704419.3
6008	15913	28040	4.74	5.6E-02	AV172708.1	EST_HUMAN	QV040606 PROTEIN ;
6241	18107	28258	2.88	5.6E-02	BE068001.1	EST_HUMAN	KY0310.s1 NCL CGAP_L2 Homo sapiens cDNA clone IMAGE:3463279.5
7110	18687	27178	2.28	5.6E-02	BE542683.1	EST_HUMAN	6010671.95F1 NH1_MGC_10 Homo sapiens cDNA clone IMAGE:3463279.5
7110	18687	27179	2.28	5.6E-02	BE542683.1	EST_HUMAN	6010671.95F1 NH1_MGC_10 Homo sapiens cDNA clone IMAGE:3463279.5
7647	17497	27719	1.15	5.6E-02	AA482884.1	EST_HUMAN	nf6607.s1 NCL CGAP_AV1 Homo sapiens cDNA clone IMAGE:923245 similar to TR.G769659 G769659
8850	18952		2.18	5.6E-02	AF200225.1	NT	LAMINA ASSOCIATED POLYPEPTIDE 1C ;
2618	12490	22375	8.16	5.6E-02	X97669.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3179	13104	22609	3.5	5.6E-02	X97669.1	NT	H. sapiens gene encoding La autoantigen
4777	14691	24448	0.91	5.6E-02	AF161265.1	NT	Mus musculus SH3 domain protein TB (SH3PDB) mRNA
5472	15352	25455	3.47	5.6E-02	Q01174	SWISSPROT	Murray Valley encephalitis virus strain WVE-1-51, complete genome
5671	15352	25456	4.31	5.6E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6305	16228	29388	1.59	5.5E-02	675902	NT	Mus musculus tubulin 1 (Tub1), mRNA
7565	17417	27632	1.3	5.5E-02	10947034	NT	Homo sapiens eIF-4E transporter (4E-T), mRNA
7565	17417	27632	1.3	5.5E-02	10947034	NT	Homo sapiens eIF-4E transporter (4E-T), mRNA
7619	17470	27689	1.48	5.5E-02	U09492.1	NT	Mus musculus second L1.1 receptor alpha chain (L1.1R2), gene, exons 1 and 2
8392	18259	28508	11.95	5.5E-02	U09771.1	NT	Citric acid (Citric acid) dehydrogenase (dhap), transcriptional activator (dhap), 1, 3-propanediol dehydrogenase (dhap), glycerol dehydrogenase (dhap)
2666	12914		0.95	5.4E-02	AJ277468.1	EST	Oryza sativa 1435-1 gene for putative Bowman Birk trypsin inhibitor
3375	16078		6.34	5.4E-02	BE078468.1	EST_HUMAN	RC5-BT0559-140200-012-003 BT0559 Homo sapiens cDNA
4968	14767	24563	0.92	5.4E-02	U03626.1	NT	Xenopus laevis homeobox protein (Vox-1), mRNA, complete cds
5108	14976	24151	1	5.4E-02	U03676.1	NT	Mus musculus p-glycoprotein (mdrla), gene, exons 1 and 2
8083	17674	28223	1.76	5.4E-02	U02705.1	NT	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8), mRNA, complete cds
8323	12524	22222	1.55	5.4E-02	U14385.1	NT	Rana catesbeiana heart shock protein 30 (HSP30), mRNA, complete cds
1037	10955	20797	1.23	5.3E-02	AW391248.1	EST_HUMAN	Q10-S10213-021290-092-009 S10213 Homo sapiens cDNA
1037	10955	20798	1.62	5.3E-02	AW391248.1	EST_HUMAN	Q10-S10213-021290-092-009 S10213 Homo sapiens cDNA
1469	11394	21255	18.21	5.3E-02	U4759.1	EST_HUMAN	h0772.11 Sinuagene lung (h077210) Homo sapiens cDNA clone (IMAGE:11954) @ similar to gb:U01590
2477	12524	22222	3.14	5.3E-02	AJ276468.1	NT	Pseudomonas putida tps gene
2812	12639	22638	3.91	5.3E-02	U09447.1	NT	Pseudomonas putida tps gene
2912	12639	22639	3.91	5.3E-02	U09447.1	NT	Drosophila melanogaster lamin B2 gene, complete cds
3113	13038	22834	4.56	5.3E-02	AJ276468.1	NT	Drosophila melanogaster lamin B2 gene, complete cds
4905	14398	24165	1.22	5.3E-02	AJ011048.1	NT	Pseudomonas putida tps gene
5021	14894	24692	7.26	6.3E-02	M01463.1	NT	Arizadopsis thaliana est gene, exons 1-11
5268	15180	24655	1.76	5.3E-02	AE000937.1	NT	Mus musculus caudal type homeobox-1 (Cdx1), gene, complete cds
5268	15180	24655	1.76	5.3E-02	AE000937.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6115	16009	26145	1.94	5.3E-02	U0984413	NT	Lymphocytic disease virus 1, complete genome
6353	16216		1.84	5.3E-02	S78221.1	NT	Nuclear protein TFI1 isoform (Nuc, mRNA, 4033 nt)
7276	17153	27149	1.76	5.3E-02	X03127.1	NT	Podopora anserina mitochondrial epsilon-sen DNA
2239	12123		439.60	5.2E-02	5031908	NT	Homo sapiens merp1a, alpha (PABA peptidyl hydrolase) (MEP1A), mRNA
3076	13003	22783	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMOT1 gene for LIM domain only 1 protein, exon 1
3076	13003	22784	2.34	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMOT1 gene for LIM domain only 1 protein, exon 1
4181	14081	23854	3.35	6.2E-02	U07132.1	NT	Human desmol hormone receptor Nef-1 mRNA, complete cds
4633	14321	24311	1.94	5.2E-02	U33246.1	NT	Drosophila melanogaster filament protein homolog (esp), gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5714	15622		1.73	5.2E-02	M30895.1	EST_HUMAN	w80d41.x1 NCL CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.61
6769	16647		2.23	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS27C004
7610	17461	27677	2.03	5.2E-02	D10922.1	NT	Turnip mosaic virus genome RNA for Capsid protein, complete cds
7610	17461	27678	2.03	5.2E-02	D10922.1	NT	Turnip mosaic virus genome RNA for Capsid protein, complete cds
9561	16157		1.63	5.2E-02	Q03030	SWISSPROT	OXYALACETATE DECARBOXYLASE ALPHA CHAIN
2313	12194	24630	1.02	5.1E-02	AL34071.1	EST_HUMAN	DKF254F0073.11 B47 (synonym: Hb57) Homo sapiens cDNA clone DK-254F0073 5'
4973	14854	24630	1.12	5.1E-02	BE967432.2	EST_HUMAN	6016635592.NH.MGC.55 Homo sapiens cDNA clone IMAGE:333361 3'
6035	15109	24971	1.85	5.1E-02	BF78625.1	EST_HUMAN	QY0100051.250800-350-408 UM0051 Homo sapiens cDNA
9056	16738	26330	1.43	5.1E-02	AL31556.1	EST_HUMAN	Spodoptera littoralis mRNA for 3-hydroxyacyl-CoA thioester reductase
7545	17433	27716	6.23	5.1E-02	AF12968.1	NT	Cardiac alkaline protein phosphatase Ss41 homolog (SSO1) gene, complete cds
7545	17689	27844	2.36	5.1E-02	P14063	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APO (PROTEIN CEX)
8204	16385	25339	2.42	5.1E-02	AF033930.1	NT	Homo sapiens ES18 mRNA, partial cds
8204	16385	25339	2.42	5.1E-02	AF033930.1	NT	Homo sapiens ES18 mRNA, partial cds
9568	16169	26234	1.81	5.0E-02	AF032467.1	NT	Oxamutic acid polyglutamate precursor (UPG3) mRNA, complete cds
474	10418	26234	1.96	5.0E-02	AF038004.1	NT	Mus musculus fatty acid synthetase gene, exon 10
1189	11050	26642	7.11	5.0E-02	Z6704.1	NT	Bacillus subtilis complete genome (section 1, 2, 3) from 1 to 21930
1847	11642		4.27	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PROSOPHOPHOREIN 12 PRECURSOR (PRP-2/PRP-4) (PRP-4/PRP-5) (PROTEIN AFPROTEIN C) [CONTAINS REPTIDE P-C]
2785	10934	20142	1.94	5.0E-02	U07842.1	NT	Cryptosporidium parvum OJD-glucuronidyltransferase (UGT2B3) mRNA, complete cds
3295	13217		1.17	5.0E-02	7309810	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (ULK2) mRNA
3029	13543	23330	6.53	5.0E-02	U17860.2	NT	Anthrax toxin protective antigen containing protein RoCn mRNA, partial cds
4890	14770	24548	0.88	5.0E-02	AF168550.1	NT	Homo sapiens ubiquitous tetrahydropteridine containing protein RoCn mRNA, partial cds
6450	16311	25477	10.61	5.0E-02	P36616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFL)
7858	17708	27954	1.32	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (FasC) mRNA, complete cds
8782	18597	28886	2.47	5.0E-02	U07690.1	NT	Methenocardine lismachil section 142 of 150 of the complete genome
9006	18563		2.81	5.0E-02	D04947	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
2118	10158		28.05	4.9E-02	M14230.1	NT	Chicken 28-40a vitamin D dependent calcium-binding protein (CaBP-28) mRNA, complete cds
5015	10321	20143	2.57	4.9E-02	AF127648.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
365	10321	20144	2.57	4.9E-02	AF127648.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3051	13174	22972	1.87	4.9E-02	P54258	SWISSPROT	ATROPHILIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3522	13438		0.87	4.9E-02	AA188940.1	EST_HUMAN	z44841.2 at Stragene NT neuron (#63723) Homo sapiens cDNA clone IMAGE:632928 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element ;
3543	13459	23262	1.10	4.9E-02	AA400914.1	EST_HUMAN	718a03.s1 Scores, bases, NNT Homo sapiens cDNA clone IMAGE:729428 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	11242	21100	2.74	4.E-02	AV172059.1	EST_HUMAN	AV172059 HTC Homo sapiens cDNA clone HTG3W.C01.6'
2438	12315	22212	2.51	4.E-02	AV173023.1	EST_HUMAN	402483.x1 NC_01_C3AP Kid11 Homo sapiens cDNA clone IMAGE:2994663 3' similar to SW:ORF1_HUMAN
2777	10235	20062	1.51	4.E-02	BE163983.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1
2977	12304	22703	0.98	4.E-02	BE163983.1	EST_HUMAN	PA0-170339-251168-003-505 HT0339 Homo sapiens cDNA
3451	12904	22703	0.95	4.E-02	BE163983.1	EST_HUMAN	PA0-170339-251168-003-505 HT0339 Homo sapiens cDNA
4033	13036	22703	1.22	4.E-02	AF220395.1	EST_HUMAN	PA0-170339-251168-003-505 HT0339 Homo sapiens cDNA
5777	15584	23792	3.84	4.E-02	X61624.1	NT	Mus musculus nuclear RNA helicase IIUG1 (c5b2.1) gene, complete cds
5777	15584	23793	3.84	4.E-02	X61624.1	NT	G.rahnerii atp2 (atp2) mRNA
6070	19093	25200	1.31	4.E-02	AJ149574.1	EST_HUMAN	nc00005.x1 Sacchar. albicans. Budwicks. 2NbpF8b9W Homo sapiens cDNA clone IMAGE:173971.3' similar to contains L1.81.1, repetitive element.
7029	16950	27097	3.95	4.E-02	BE164063.1	EST_HUMAN	PA0-170339-251168-003-505 HT0339 Homo sapiens cDNA
8707	18524	28806	3.38	4.E-02	AA913328.1	EST_HUMAN	GP1093.x1 Sacchar. NE_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1824737.3'
8963	19738		1.34	4.E-02	L11692.1	NT	Cryptosporidium parvum mRNAs encoding a sporozoite type II mRNA, complete cds
8945	19343		2.88	4.E-02	X67808.1	NT	Human gamma interferon mRNA, complete cds
439	10383	20207	1.84	4.E-02	P22248.1	SWISSPROT	PEP1NOC ACID RECEPTOR BETA (RA5-BETA)
1200	11110	20955	0.85	4.E-02	AF005790.1	NT	Human gamma interferon mRNA, complete cds
1200	11110	20956	0.85	4.E-02	AF005790.1	NT	Human gamma interferon mRNA, complete cds
1768	11682	21535	3.45	4.E-02	P32762	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
2003	11963	21830	2.04	4.E-02	AE003964.1	NT	Xylella fastidiosa, section 110 of 229 of the complete genome
3692	13576	23384	3.83	4.E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5778	15685	25764	1.54	4.E-02	AJ400877.1	NT	Homo sapiens ASCL3 gene, C6orf14 gene, C11orf16 gene and C11orf17 gene
6801	16770	25665	2.3	4.E-02	AF006884.1	NT	Arabidopsis thaliana CCNAAT-box binding factor P-AP3 homolog gene, complete cds
7718	17568	27793	4.43	4.E-02	AA325216.1	EST_HUMAN	EST28167 Cerebellum I Homo sapiens cDNA 5' end similar to neuro-D4 protein
9301	19000	29331	1.74	4.E-02	11418019	NT	Homo sapiens rat finger protein-like 5 (RFLP3), mRNA
6691	19637	25009	3.41	4.E-02	AA191097.1	EST_HUMAN	zfx311.11 Striatagene NT neuron (8937233) Homo sapiens cDNA clone IMAGE:632493.5'
213	10184		4.79	4.E-02	BE091273.1	EST_HUMAN	GP1692154F1 NT_MGC_92 Homo sapiens cDNA clone IMAGE:3935388.5'
1008	10029	20770	1.26	4.E-02	L16295.1	NT	Drosophila melanogaster extracellular (EXO) mRNA, complete cds
2049	11940		6.15	4.E-02	P31569	SWISSPROT	HYPOPHYSAL PROTEIN (ORF 2280)
2440	12317	22214	1.29	4.E-02	AW576475.1	EST_HUMAN	QV2-P10012101000-070-g02 PT0012 Homo sapiens cDNA
3698	18902	23291	1.88	4.E-02	AF169100.1	NT	Myococcum xanthus serine/threonine kinase Ptk10 (p1010) gene, complete cds
4527	14420		1.08	4.E-02	AF109807.1	NT	Homo sapiens S164 gene, partial cds; PS1 and tyrosinase protein genes, complete cds; and S171 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit ELAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3824	13736	23327	0.89	4.1E-02	BC287236.1	EST_HUMAN	801175071.NH_MGC_17 Homo sapiens cDNA clone IMAGE3530358
4372	14268		7.37	4.1E-02	AU1893484.1	EST_HUMAN	QV-HN0012-180400-164-08 HN0012 Homo sapiens cDNA
8436	16297	28450	1.94	4.1E-02	7692927.1	NT	Homo sapiens KIA00867 protein (KIA00867), mRNA
6565	16423	26954	2.44	4.1E-02	AF0261193.1	NT	Fugu subtypes neural cell adhesion molecule 1 (NCAM) gene, complete cds; palliative protein 1 (PUT1) gene, partial cds; mitotic-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8873	16832	24694	12.83	4.1E-02	AJ271909.1	NT	Banana rapus chi gene for plastid glutamine synthetase, exon 1-12
3206	13130	22362	2.66	4.0E-02	AB040394.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
5304	15225	26026	4.32	4.0E-02	AF260107.1	NT	Homo sapiens cytochrome P450 polypeptide A5 (CYP2A4.5) gene, partial cds; cytochrome P450 polypeptide 4 (CYP2A4) gene, partial cds; cytochrome P450 polypeptide 7 (CYP2A7) gene, complete cds; and cytochrome P450 polypeptide 5 (CYP2A5) gene, partial cds
8628	16387	25897	5.98	4.0E-02	Z6388.1	NT	Synglucosaminiduria peruraria homolog of human bone morphogenetic protein 1 (ubmp) mRNA, complete cds
7059	16696	27126	2.8	4.0E-02	P06640	SWISSPROT	GLUCOXYMUTASE S192 PRECURSOR (GLUCAN Y 1,4-ALPHA-D-GLUCOSYLASE)
7572	17423	-27638	2.42	4.0E-02	AJ000941.1	NT	Methanococcus thermotrophicum strain Marburg, Thick/thin-layered reductase subunit A
8883	16788		1.94	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Cas+ ATPase
9169	16900	25135	4.96	4.0E-02	AJ001096.1	NT	Osteoarthritis-like gene for Csp+/ATPase
1104	11020	20063	2.71	3.8E-02	BF519149.1	EST_HUMAN	JFH-BWT-amk-h8-QJ1st1 NC1_GGAP_Sub7 Homo sapiens cDNA clone IMAGE3081343
3322	11220	21084	3.48	3.9E-02	PA14147	SWISSPROT	FAS ANTIGEN LIQUANT
1918	11811	21691	3.04	3.9E-02	AJ403360.1	NT	Musculus DNA for desmin-binding fragment D627
2671	12536		2.26	3.9E-02	4596802	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15KD (SDHC) mRNA
5105	14973	24748	0.96	3.9E-02	8924016	NT	Homo sapiens hypodermal protein PRO1181 (PRD1183), mRNA
5105	14973	24748	0.96	3.9E-02	8924016	NT	Homo sapiens hypodermal protein PRO1181 (PRD1183), mRNA
5591	16461	26564	1.22	3.9E-02	BF236513.1	EST_HUMAN	801608465.NH_MGC_54-Homo sapiens cDNA clone IMAGE4184779.5
9058	18544		5.45	3.9E-02	AQ042553.1	NT	Felis catus G-CcSF gene for granulocyte colony-stimulating factor, complete cds
9887	19248		1.57	3.9E-02	U66091.1	EST_HUMAN	Human germ-line T-cell receptor beta chain TORB/17S1A1T, TORBV/2S1, TORBV/10S1P, TORBV/29S1P, TORBV/10S1P, TORBV/15S1T, HVB relc, TORBV/28S1P, TORBV/34S1, TORBV/14S1, TORBV/3S1, TORBV/4S1T, TRY4, TRY6, TRY7, TORBD1, TORBJ1S1, TORBJ1S2, TORBJ1S3, TORBJ1S4, TORBJ1S5, TORBJ1S6, TORBJ1S7, TORBJ1S8, TORBJ1S9, TORBJ1S10, TORBJ1S11, TORBJ1S12, TORBJ1S13, TORBJ1S14, TORBJ1S15, TORBJ1S16, TORBJ1S17, TORBJ1S18, TORBJ1S19, TORBJ1S20, TORBJ1S21, TORBJ1S22, TORBJ1S23, TORBJ1S24, TORBJ1S25, TORBJ1S26, TORBJ1S27, TORBJ1S28, TORBJ1S29, TORBJ1S30, TORBJ1S31, TORBJ1S32, TORBJ1S33, TORBJ1S34, TORBJ1S35, TORBJ1S36, TORBJ1S37, TORBJ1S38, TORBJ1S39, TORBJ1S40, TORBJ1S41, TORBJ1S42, TORBJ1S43, TORBJ1S44, TORBJ1S45, TORBJ1S46, TORBJ1S47, TORBJ1S48, TORBJ1S49, TORBJ1S50, TORBJ1S51, TORBJ1S52, TORBJ1S53, TORBJ1S54, TORBJ1S55, TORBJ1S56, TORBJ1S57, TORBJ1S58, TORBJ1S59, TORBJ1S60, TORBJ1S61, TORBJ1S62, TORBJ1S63, TORBJ1S64, TORBJ1S65, TORBJ1S66, TORBJ1S67, TORBJ1S68, TORBJ1S69, TORBJ1S70, TORBJ1S71, TORBJ1S72, TORBJ1S73, TORBJ1S74, TORBJ1S75, TORBJ1S76, TORBJ1S77, TORBJ1S78, TORBJ1S79, TORBJ1S80, TORBJ1S81, TORBJ1S82, TORBJ1S83, TORBJ1S84, TORBJ1S85, TORBJ1S86, TORBJ1S87, TORBJ1S88, TORBJ1S89, TORBJ1S90, TORBJ1S91, TORBJ1S92, TORBJ1S93, TORBJ1S94, TORBJ1S95, TORBJ1S96, TORBJ1S97, TORBJ1S98, TORBJ1S99, TORBJ1S100, TORBJ1S101, TORBJ1S102, TORBJ1S103, TORBJ1S104, TORBJ1S105, TORBJ1S106, TORBJ1S107, TORBJ1S108, TORBJ1S109, TORBJ1S110, TORBJ1S111, TORBJ1S112, TORBJ1S113, TORBJ1S114, TORBJ1S115, TORBJ1S116, TORBJ1S117, TORBJ1S118, TORBJ1S119, TORBJ1S120, TORBJ1S121, TORBJ1S122, TORBJ1S123, TORBJ1S124, TORBJ1S125, TORBJ1S126, TORBJ1S127, TORBJ1S128, TORBJ1S129, TORBJ1S130, TORBJ1S131, TORBJ1S132, TORBJ1S133, TORBJ1S134, TORBJ1S135, TORBJ1S136, TORBJ1S137, TORBJ1S138, TORBJ1S139, TORBJ1S140, TORBJ1S141, TORBJ1S142, TORBJ1S143, TORBJ1S144, TORBJ1S145, TORBJ1S146, TORBJ1S147, TORBJ1S148, TORBJ1S149, TORBJ1S150, TORBJ1S151, TORBJ1S152, TORBJ1S153, TORBJ1S154, TORBJ1S155, TORBJ1S156, TORBJ1S157, TORBJ1S158, TORBJ1S159, TORBJ1S160, TORBJ1S161, TORBJ1S162, TORBJ1S163, TORBJ1S164, TORBJ1S165, TORBJ1S166, TORBJ1S167, TORBJ1S168, TORBJ1S169, TORBJ1S170, TORBJ1S171, TORBJ1S172, TORBJ1S173, TORBJ1S174, TORBJ1S175, TORBJ1S176, TORBJ1S177, TORBJ1S178, TORBJ1S179, TORBJ1S180, TORBJ1S181, TORBJ1S182, TORBJ1S183, TORBJ1S184, TORBJ1S185, TORBJ1S186, TORBJ1S187, TORBJ1S188, TORBJ1S189, TORBJ1S190, TORBJ1S191, TORBJ1S192, TORBJ1S193, TORBJ1S194, TORBJ1S195, TORBJ1S196, TORBJ1S197, TORBJ1S198, TORBJ1S199, TORBJ1S200, TORBJ1S201, TORBJ1S202, TORBJ1S203, TORBJ1S204, TORBJ1S205, TORBJ1S206, TORBJ1S207, TORBJ1S208, TORBJ1S209, TORBJ1S210, TORBJ1S211, TORBJ1S212, TORBJ1S213, TORBJ1S214, TORBJ1S215, TORBJ1S216, TORBJ1S21

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6331	16184	26345	1.74	3.9E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABC8), mRNA
7033	18910	28185	1.39	3.9E-02	M0076.1	NT	Human von Willebrand factor gene, exons 23 through 34
8046	17693	28185	2.45	3.9E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
976	10669	20746	4.59	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-7 CHAIN PRECURSOR (LAMININ A CHAIN)
1366	11272	21128	0.9	3.7E-02	L14691.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2190	12077	21932	6.3	3.7E-02	AF694006.1	EST_HUMAN	wf5503.x1 NO1 CGAP K6H1 Homo sapiens cDNA clone IMAGE:2194502.3
2633	12407	22269	0.61	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0716 protein, partial cds
3012	12940	22733	0.8	3.7E-02	P76944	SWISSPROT	EMESODERMIN
3013	12941	22734	3.45	3.7E-02	BF312693.1	EST_HUMAN	00180233F1 NH1.MGC. 19 Homo sapiens cDNA clone IMAGE:412584.5
3408	13325		1.1	3.7E-02	6930541	NT	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnnk3), mRNA
5095	18997	26119	3.4	3.7E-02	BF124974.1	EST_HUMAN	001762117F1 NH1.MGC. 20 Homo sapiens cDNA clone IMAGE:4024973.5
5755	19536	26093	1.62	3.7E-02	11418362	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3604	13518	23306	0.85	3.9E-02	X7321.1	NT	H. vulgare S-1 gene for succinate synthase
3612	13526	23313	0.8	3.9E-02	AL099008.1	NT	Homo sapiens genomic region containing type-variable minisatellites chromosomes 10 (10q28.3) of Homo sapiens
5195	19002	24773	0.84	3.9E-02	AL099010.1	NT	Homo sapiens genomic region containing type-variable minisatellites chromosomes 10 (10q28.3) of Homo sapiens
8028	19932	26002	5	3.9E-02	AF1945916.1	EST_HUMAN	CH2-EN0013-11050-192510 EN0013 Homo sapiens cDNA
8028	19932	26003	5	3.9E-02	AF1945916.1	EST_HUMAN	CH2-EN0013-11050-192510 EN0013 Homo sapiens cDNA
8214	19000	26229	1.82	3.9E-02	AF029532.1	NT	Chromatium viscum sulfur globule protein C2 precursor (gcp2) gene, complete cds
8324	16187	26349	2.63	3.9E-02	AA714621.1	EST_HUMAN	HW2005.s1 NO1 CGAP GCB0 Homo sapiens cDNA clone IMAGE:1211024.3 similar to gb:00314_m02 TUBULIN BETA-1 CHAIN (HUMAN)
7402	17269	27473	2.08	3.9E-02	U06008.1	NT	Dicystidium discoidum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
7402	17269	27474	2.08	3.9E-02	U06008.1	NT	Dicystidium discoidum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
867	10803	20693	1.15	3.9E-02	U06006.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
992	10913	20786	1.53	3.9E-02	AF283417.1	NT	Homo sapiens microosomal epoxide hydrolase (EPHX1) gene, complete cds
1544	11449	21309	1.49	3.9E-02	BF678005.1	EST_HUMAN	00206519F1 NH1.MGC. 83 Homo sapiens cDNA clone IMAGE:4268377.5
1544	11449	21310	1.49	3.9E-02	BF678005.1	EST_HUMAN	00206519F1 NH1.MGC. 83 Homo sapiens cDNA clone IMAGE:4268377.5
4120	14020	23798	2.01	3.9E-02	AE001773.1	NT	Thermoboga maritima section 65 of 136 of five complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4220	14118	23895	1.43	3.9E-02	P83780	SWISSPROT	CYSTITHIONINE BETA-LYASE PRECURSOR (CSL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
4836	14429		0.66	3.9E-02	AW959469.1	EST_HUMAN	EST1370639 IMAGE rescues, IMAGE Homo sapiens cDNA
9154	15021		0.84	3.9E-02	P47144	SWISSPROT	HYPOHETICAL 80.7 KD PROTEIN IN SODIUM-DEPENDENT INTERGENIC REGION
6773	15980	25787	1.88	3.9E-02	J01238.1	NT	Mtze actin 1 gene (Mact1), complete cds
7012	16889	27082	2.35	3.9E-02	BC589970.1	EST_HUMAN	801644701R2 NIH_MGC_596 Homo sapiens cDNA clone IMAGE:38259737 3'
7785	17605	27829	1.72	3.9E-02	X76542.1	EST	Lactica MG1363 gfpE and drak genes
8785	18600	28859	1.76	3.9E-02	AW861641.1	EST_HUMAN	PM1-C103235-291259-002-003 CT0326 Homo sapiens cDNA
9749	19592	29830	1.79	3.9E-02	AW861641.1	EST_HUMAN	PM1-C103235-291259-002-003 CT0326 Homo sapiens cDNA
594	19594	29310	1.78	3.9E-02	AK024424.1	NT	801178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
594	19594	29311	1.78	3.9E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
595	19594	29310	3.31	3.9E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
595	19594	29311	3.31	3.9E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1035	10953	20795	3.77	3.4E-02	AW274020.1	EST_HUMAN	XG9407.v1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814263 3' similar to
1188	11098		10.22	3.4E-02	11545456	NT	SW_C211_HUMAN P33901 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ; Homo sapiens hypothetical protein FLJ13320 (FLJ13320), mRNA
2343	12223	22120	2.05	3.4E-02	T57160.1	EST_HUMAN	p320a6.1 Stradiene lung (493720) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains
3834	13302	23103	1.28	3.4E-02	AL103208.2	NT	MEP29 regulatory element
3709	13822	23405	1.07	3.4E-02	BC589514.1	EST_HUMAN	Homo sapiens chromosome 21, segment H521 C008
3875	13759	23550	3.19	3.4E-02	AW179492.1	EST_HUMAN	RC3-FN0155-060700-011-410 FN0155 Homo sapiens cDNA
4494	14388	24174	2.41	3.4E-02	X97884.1	NT	IG2-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4962	14857		3.43	3.4E-02	C29685.1	SWISSPROT	Musculus Strangien gene promoter region
5070	14884	24690	1.28	3.4E-02	A012409.1	NT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5095	15105	24898	4.19	3.4E-02	U24393.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6908	16857		4.78	3.4E-02	AB60259.1	EST_HUMAN	Human liver oligodendrocyte-like protein genes, exon 3
							W6604LX1 NCI_GDAP Brn25 Homo sapiens cDNA clone IMAGE:2435031 3'
							zfp471.1 Stradiene muscle 837209 Homo sapiens cDNA clone IMAGE:626749 3' similar to
							IR-G1017425 G1017425
7199	17046		6.07	3.4E-02	AA184306.1	EST_HUMAN	IPISGKLPKLVLSIOGVPLKATMRNTTEAINTLNKESTVADAGRYETAANSSGTAKFNWILDRPG
398	10324		13.18	3.9E-02	AA389673.1	EST_HUMAN	PPT GPWISDSITSEVLKWPFKYDGSQVYNLLKKEISTAVTVEYSVARTAMKMKVKL ... ;
1151	11064	20907	13.17	3.9E-02	AB039597.1	NT	275608.v1 Scores: Insulin_NHT Homo sapiens cDNA clone IMAGE:728168 3'
1021	11525	21383	1.08	3.9E-02	AF110783.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P-450 2A17, complete cds
							Homo sapiens skeletal muscle LIM-protein 1 (P-L1) gene, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1705	11606		1.28	3.3E-02	AE000700.1	NT	Aquifer aeliscus section 32 of 105 of the complete genome
2038	11929		2.77	3.3E-02	R09112.1	EST_HUMAN	YF509.0.1 Scores: total liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:17688.5'
4086	11526	21383	2.24	3.3E-02	AF1107.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (PHL1) gene, complete cds
4396	14262	20477	1.88	3.3E-02	675982.1	EST_HUMAN	Mus musculus skeletal muscle rejection antigen gp95 (Trst1) mRNA
5875	13761	25601	18.26	3.3E-02	BF245696.1	EST_HUMAN	601853010F1 NH1_MGC_57 Homo sapiens cDNA clone IMAGE:4073787.5'
5875	15781	25602	18.26	3.3E-02	BF245696.1	EST_HUMAN	60224717F1 NH1_MGC_57 Homo sapiens cDNA clone IMAGE:4073787.5'
8494	18337	28601	3.39	3.3E-02	BF691107.1	EST_HUMAN	60224717F1 NH1_MGC_57 Homo sapiens cDNA clone IMAGE:4332467.5'
9290	19591		1.78	3.3E-02	TG9545.1	EST_HUMAN	ye4671.1.1 Scores: total liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:121101.5'
9441	19078		1.69	3.3E-02	M81850.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
127	10101	19523	1.13	3.2E-02	AJ002005.1	NT	Oryzopsis cuniculatus gene encoding liver sodium-dependent bile acid transporter
1110	11025	20687	12.7	3.2E-02	AF056275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hap88d allele, complete cds
1110	11025	20688	12.7	3.2E-02	AF056275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hap88d allele, complete cds
1734	11635	21503	1.14	3.2E-02	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TER) gene, exons 7-19 and complete cds
2072	11682	0.91	0.91	3.2E-02	F28895.1	SWISSPROT	LARGE TEGUMENT PROTEIN
2859	10101	19523	1.16	3.2E-02	AJ002005.1	NT	Oryzopsis cuniculatus gene encoding liver sodium-dependent bile acid transporter
3035	13022	22817	10.71	3.2E-02	BE607383.1	EST_HUMAN	80144243.F1 NH1_MGC_66 Homo sapiens cDNA clone IMAGE:3846727.5'
3653	13597	23334	1.05	3.2E-02	AF149383.2	NT	Homo sapiens chromosome 21 segment HS21C003
4124	14024		12.36	3.2E-02	X67478.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4658	14544	24333	2.88	3.2E-02	AF114182.1	NT	Saccharomyces cerevisiae (baker's yeast) gene encoding chloroplast protein, pericid cds
5359	15318	25595	1.46	3.2E-02	X68709.1	NT	S.griecococcum wild-SIV gene
5359	15318	25596	1.46	3.2E-02	X68709.1	NT	S.griecococcum wild-SIV gene
5651	16596	25699	2.26	3.2E-02	M62437.1	NT	Ratp10minous left function in cell line W88.14
5652	16637		26.54	3.2E-02	T63067.1	EST_HUMAN	y43812.5.1 Scores: total liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:110087.3' similar to contains
5696	18661	20013	3.72	3.2E-02	AF173845.1	NT	Alu repetitive element contains LTR1 repetitive element
6830	16709	25902	3.46	3.2E-02	6930565	NT	Saguinus oedipus tissue kallikrein gene, complete cds
7796	17036		3.82	3.2E-02	A4749795.1	EST_HUMAN	2946412.5.1 Scores: thymal gland, NHSPG Homo sapiens cDNA clone IMAGE:397151.3' similar to
9952	13487		1.38	3.2E-02	AE021084.1	NT	gpl08441 CYTOCHROME C OXIDASE POLYPEPTIDE II (HUMAN)
1239	11146		2.05	3.1E-02	4903416	NT	Marchantia polymorpha gene for 26S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
1283	11191	21043	1.26	3.1E-02	P16845	SWISSPROT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
1850	11746	21621	1.09	3.1E-02	6671954	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1931	11826		1.35	3.1E-02	Z80097.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Apo3), mRNA
							Drosophila melanogaster mRNA for headcase protein

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon ID NO.	Offc SEQ ID NO.	Expression Signal	Mean Signal (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4152	14052		0.82	3.1E-02	AU116006.1	EST_HUMAN	AU116006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
4767	14652	24440	0.98	3.1E-02	AV183513.1	EST_HUMAN	QV0-L70014-250200-128-H08L10014 Homo sapiens cDNA
5290	15211		2.33	3.1E-02	A4278478.1	EST_HUMAN	z881066.r1 NCL_GCAP GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
7765	17615	27843	2.82	3.1E-02	AF094779.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1606	11511		2.82	3.0E-02	AF187125.1	NT	Phoklaia minuta oxyphosphatase (gene, partial cds, mitochondrial, gene for mitochondrial product
2541	12415	22305	1.07	3.0E-02	A4402242.1	EST_HUMAN	z85903.r1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:272265 5'
3518	13454	2324	1.07	3.0E-02	A044784.1	NT	Pseudomonas aeruginosa stem-loop mutation suppressor SSI.2, gene, complete cds
3603	13671	23305	2.81	3.0E-02	AF247844.1	EST_HUMAN	Pseudomonas fluorescens family II (anthranilate synthase gene, complete cds
3695	13598		0.98	3.0E-02	A1362023.1	EST_HUMAN	QV2-310289-160200-040-029 S10295 Homo sapiens cDNA
3895	13777		1.18	3.0E-02	A1364003.1	EST_HUMAN	EST14530 Pinald, gland II Homo sapiens cDNA 5' and
4778	14657	24444	0.89	3.0E-02	BE782630.1	EST_HUMAN	601472331.F1 NH_MGC_07 Homo sapiens cDNA clone IMAGE:3875693 5'
4833	14858	24624	6.02	3.0E-02	AF251074.1	NT	Homo sapiens neuropilin-2 (NRP-2) gene, complete cds, alternatively spliced
5312	12533	24625	6.02	3.0E-02	AF251074.1	NT	Homo sapiens neuropilin-2 (NRP-2) gene, complete cds, alternatively spliced
5312	12533		2.88	3.0E-02	AB040763.1	NT	Homo sapiens mRNA for KIAA1373 protein, partial cds
6095	16050	28196	2.71	3.0E-02	AJ242905.1	NT	Cyprinina carpio mRNA for inducible nitric oxide synthase (NOS gene)
6127	16974	28198	3.38	3.0E-02	BE886948.1	EST_HUMAN	601512206.F1 NH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6127	16974	28110	3.38	3.0E-02	BE886948.1	EST_HUMAN	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete
6207	16967	28101	1.79	3.0E-02	AF210884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete
6207	16967	28102	1.79	3.0E-02	AF210884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete
6292	19150	28311	1.54	3.0E-02	IM86524.1	NT	Human oxyphosphatase gene
7106	10983		2.11	3.0E-02	AF275654.1	NT	Onchitrichus asellus coagulation factor X mRNA, complete cds
7878	17828	28080	1.71	3.0E-02	AF001187.1	NT	Thermolago maritima section 109 of 136 of the complete genome
8592	18432	28091	3.06	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
8937	18745	28093	7.7	3.0E-02	A4483216.1	EST_HUMAN	nef7004.s1 NCL_GCAP Kd1 Homo sapiens cDNA clone IMAGE:571263
9396	19730	24659	1.86	3.0E-02	R23016.1	EST_HUMAN	nef7004.s1 Soares Phenotype N282P Homo sapiens cDNA clone IMAGE:194407 3'
9740	19273		4.87	3.0E-02	AV186595.1	EST_HUMAN	QV4-NN0038-270400-187-403 NN0038 Homo sapiens cDNA
9790	19723		2.06	3.0E-02	AF046987.1	NT	Rattus norvegicus UDP-Galactose 4-epimerase mRNA, complete cds
2395	12720	22157	1.1	2.9E-02	AF2726703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytochrome c oxidase subunit 1 (COX1) gene, complete cds, alternatively spliced
2592	12869	22987	1.07	2.9E-02	BE595944.1	EST_HUMAN	601339422.F1 NH_MGC_53 Homo sapiens cDNA clone IMAGE:380665 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Htt BLAST Value	Top Htt Accession No.	Top Htt Database Source	Top Htt Description
28202	12889	22888	1.07	2.9E-027	BE590644.1	EST	HUMAN
3881	13762	23195	0.92	2.8E-027	BT172003.1	EST	HUMAN
4950	14827	24593	1.32	2.9E-027	X051937.1	NT	S. vulgaris pepC gene for PEP carboxylase
4950	14827	24594	1.32	2.9E-027	X051937.1	NT	S. vulgaris pepC gene for PEP carboxylase
5759	16705	25817	10.37	2.9E-027	BF022233.1	EST	HUMAN
6256	16762	26319	8.43	2.9E-027	BF022437.1	EST	HUMAN
7568	17419	27635	1.94	2.9E-027	AF1676976.1	EST	HUMAN
7568	17419	27636	1.94	2.9E-027	AF1676976.1	EST	HUMAN
553	18344	28043	0.87	2.8E-027	AF020153.1	EST	HUMAN
3321	13241	23048	1.37	2.8E-027	AF060083.1	NT	Homo sapiens retinal facin (FSCN2) gene, exon 2
3321	13241	23047	1.27	2.8E-027	AF060083.1	NT	Homo sapiens retinal facin (FSCN2) gene, exon 2
4214	14121		0.98	2.8E-027	BC83761	NT	Putative non-muscle myosin-like-associated protein Aa (MyoA) mRNA
5373	15293	25740	11.41	2.9E-027	BE711083.1	EST	HUMAN
6547	16724	26920	1.33	2.8E-027	AF000862.1	NT	Chlorodioxa phenanthrene mRNA for homodimeric lauric acid zipper protein (hcl-1)
6674	16774		1.51	2.8E-027	R006861	EST	HUMAN
9880	18237		1.33	2.8E-027	X06322.1	NT	Yeast CNU30 chromosome III RARS DNA (right arm transcription hot-spot)
1473	11378	21242	1.26	2.7E-027	U66050.1	NT	Human gamma T cell receptor beta chain Dopamine-beta-hydroxylase-like, TRV1, TRV2, TRV3, TORB6V57SP, TORB6V251A2NT, TORB6V51A1T, TORB6V591A1T, TORB6V333, TORB6V657P, TORB6V73A2T, TORB6V352A1T, TORB6V52A2P1T, TORB6V792A1N4T, TORB6V13581B3A2
3385	13303	23103	2	2.7E-027	AF161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4107	14007	23783	2.07	2.7E-027	AF161494.2	EST	HUMAN
4107	14007	23784	2.07	2.7E-027	N47258.1	EST	HUMAN
6205	15895	26109	1.19	2.7E-027	AF160657.1	EST	HUMAN
6946	16530	28134	1.32	2.7E-027	BF514658.1	EST	HUMAN
556	10450	23035	1.14	2.7E-027	AF163292.2	NT	Homo sapiens chromosome 21 segment HS21C082
1345	11251		1.04	2.8E-027	AF163292.1	EST	HUMAN
2341	12159	22009	2.19	2.8E-027	AF4800915.1	EST	HUMAN
2341	12159	22008	2.86	2.8E-027	AF4800915.1	EST	HUMAN
2317	12198	22016	2.86	2.8E-027	6764241	NT	Mus musculus histidine rich calcium binding protein (Hrc) mRNA
2317	12198	22005	2.86	2.8E-027	6764241	NT	Mus musculus histidine rich calcium binding protein (Hrc) mRNA
2885	12812		1.95	2.8E-027	AF106003.1	NT	Mus musculus MHC class II region DR gene, partial cds; B1, C2, GAA, NG22, G6, HSP70, HSP70, HSC70H, and aMNP genes, complete cds; G7A gene, partial cds; and unknown genes
3893	13704		1.13	2.8E-027	AF161045.1	EST	HUMAN
4517	14410		1.13	2.8E-027	BE598892.1	EST	HUMAN
4517	14410		1.13	2.8E-027	BE598892.1	EST	HUMAN

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4811	14065	24481	3.69	2.6E-02	L12032.1	NT	Chicken dorsal-l1 mRNA, complete cds
4998	14873	24637	1.67	2.6E-02	AF02014.1	NT	Dichococcus radiodurans R1 section 151 of 228 of the complete chromosome 1
5025	14898	24697	2.06	2.6E-02	AW241154.1	EST_HUMAN	h232004.x1 NCL CGAP_S44 Homo sapiens cDNA clone IMAGE:2570933 3' similar to SW:7069_HUMAN
5771	15678		0.95	2.6E-02	A120030.1	EST_HUMAN	Q16041 HYPOTHETICAL PROTEIN KIAA0089 ;
6570	15776	25895	2.08	2.6E-02	BE521748.1	EST_HUMAN	q27217.x1 NCL CGAP_K48 Homo sapiens cDNA clone IMAGE:1762317 3'
6130	15977	26113	6.09	2.6E-02		EST_HUMAN	60148347311 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895978 3'
7398	17300	27512	1.19	2.6E-02	608127	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7548	17768	28038	4.87	2.6E-02	A113303.2	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
8502	18576		2.1	2.6E-02	AA276351.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
8848	18690	28949	1.86	2.6E-02	AV30047.1	EST_HUMAN	z84402.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704182 5'
6320	19016	24605	1.55	2.6E-02	AF343927.1	EST_HUMAN	U1HF-BNO-484-e-10-0-UL11 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077466 5'
5211	19463	20274	1.45	2.6E-02	AF33130.1	EST_HUMAN	602015501F1 NCL CGAP_Bln64 Homo sapiens cDNA clone IMAGE:4150944 5'
5211	19463	20275	1.45	2.6E-02	AF33130.1	EST_HUMAN	nc2806.v6 NCL CGAP_L46 Homo sapiens cDNA clone IMAGE:1577627 5'
7021	10721	20582	12.83	2.6E-02	BE074314.1	EST_HUMAN	60158035622 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950965 3'
651	10761	20628	4.37	2.6E-02	BE074314.1	EST_HUMAN	60158035622 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950965 3'
2738	12937		2.86	2.6E-02	U12371.1	NT	Rattus norvegicus ribophorin-3A, mRNA, complete cds
2628	12853	22882	4.4	2.6E-02	X65927.1	NT	H. sapiens mRNA for luciferase, chlorophyll a/b binding protein, Fcp1
2828	12853		4.4	2.6E-02	X65927.1	NT	H. sapiens mRNA for luciferase, chlorophyll a/b binding protein, Fcp1
3369	19070	23643	1.09	2.6E-02	BE0701165.1	EST_HUMAN	FL42-NN0723-00070-001-472 NN0728 Homo sapiens cDNA
3659	19070	23644	1.09	2.6E-02	BE0701165.1	EST_HUMAN	FL42-NN0723-00070-001-472 NN0728 Homo sapiens cDNA
4111	14011	23768	5.07	2.6E-02	AW562114.1	EST_HUMAN	h232004.x1 Soares_NFL_1_GCC_S1 Homo sapiens cDNA clone IMAGE:3264008 3' similar to L1:11 L1
5799	15687		4.48	2.6E-02	BE670728.1	EST_HUMAN	repulsive element ;
5797	15674		3.86	2.6E-02	BE74688.1	EST_HUMAN	6015753933F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:3928654 5'
6519	16378	20555	1.57	2.6E-02	BF520722.1	EST_HUMAN	6020705625F1 NCL CGAP_Bln64 Homo sapiens cDNA clone IMAGE:4213406 5'
6519	16378	20556	1.57	2.6E-02	BF520722.1	EST_HUMAN	6020705625F1 NCL CGAP_Bln64 Homo sapiens cDNA clone IMAGE:4213406 5'
8185	18071	28320	2.45	2.6E-02	Q10335	SWISSPROT	HYPOTHETICAL 467 KD PROTEIN C18G10.05 IN CHROMOSOME 1
8185	18071	28321	2.45	2.6E-02	Q10335	SWISSPROT	HYPOTHETICAL 467 KD PROTEIN C18G10.05 IN CHROMOSOME 1
8238	18178	28370	3.38	2.6E-02	AJ237936.1	NT	Eco stauris partial stauB gene, exons 17-19
8295	18135		3.33	2.6E-02	AF090157.1	NT	Mus musculus major histocompatibility locus class II region; major histocompatibility protein class II alpha chain (A2alpha) and major histocompatibility protein class II beta chain (E2beta) genes, complete cds;
8978	18763		1.74	2.6E-02	AB007548.1	NT	Myoophelin-like (NC9), myoophelin-lb
							Homo sapiens gene for LECT2, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
829C	19557		2.19	2.1E-02	1142078	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9403	19528		1.63	2.1E-02	1143329	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9591	19167	28271	2.30	2.1E-02	BE973327.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
1077	10139	19056	1.01	2.4E-02	A1378582.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
1500	11484	21344	1.80	2.4E-02	H65894.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
1998	12710	21784	2.22	2.4E-02	PC1901	SWISSPROT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
1998	12710	21785	2.22	2.4E-02	PC1901	SWISSPROT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
4372	14171	23048	1.4	2.4E-02	J6510.1	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
4372	14314	24099	1.43	2.4E-02	PC1901	SWISSPROT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
4372	14314	24100	1.43	2.4E-02	PC1901	SWISSPROT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
5119	14877		1.151	2.4E-02	AL161955.2	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9902	18640	27092	10.36	2.4E-02	N8942.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
7843	17493	27714	2.17	2.4E-02	AF62554.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
7794	17564	27908	2.96	2.4E-02	AA46894.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
8857	18689	28869	1.86	2.4E-02	AF16905.1	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
8857	18689	28869	1.86	2.4E-02	AF16905.1	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
8090	18656		1.95	2.4E-02	6827009	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9224	18847	28357	2.72	2.4E-02	6753635	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9282	18884	28526	2.03	2.4E-02	BE926990.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
6398	18036		1.27	2.4E-02	AF163864.1	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9505	19120		3.87	2.4E-02	AB008569.1	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9532	19138		1.6	2.4E-02	N42860.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9538	19141		1.38	2.4E-02	BF78477.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
9077	19887		1.99	2.4E-02	PC5453	SWISSPROT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
1820	11726		5.78	2.3E-02	W05340.1	EST_HUMAN	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
1844	11740		7.86	2.3E-02	U94165.1	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA
2802	12183	22081	2.82	2.3E-02	Z74933.1	NT	Homo sapiens similar to ALEXO protein (H. sapiens) (LOC83894), mRNA

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3844	13735	23549	0.95	2.2E-02	274293.1	NT	S cerevisiae chromosome IV reading frame ORF YOL245c
6977	16161	26318	3.78	2.2E-02	AV665721.1	EST_HUMAN	AV665721 GK6 Homo sapiens cDNA clone GK6ND03 3'
6978	16755	26942	2.26	2.2E-02	AL161515.2	NT	Anhidrosis thalassia DNA chromosome 4, contig fragment No. 27
6876	16755	26953	2.26	2.2E-02	AL161515.2	NT	Anhidrosis thalassia DNA chromosome 4, contig fragment No. 27
7595	17436	27651	2.33	2.2E-02	AB026958.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
7595	17436	27652	2.33	2.2E-02	AB026958.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9408	18366		2.24	2.2E-02	AA593553.1	EST_HUMAN	ncf7407 s1 NCI_CGAP_Co8 Homo sapiens cDNA clone MDSADG01 5'
413	10339		5.66	2.1E-02	AV761502.1	EST_HUMAN	AV761502 M3S Homo sapiens cDNA clone MDSADG01 5'
441	10351		7.99	2.1E-02	AF026728.1	NT	Dichroptolium discoloratum histidine kinase C (DNC) mRNA, complete cds
1242	11148	20983	7.45	2.1E-02	U72073.1	NT	Bacillus subtilis coxIIIM cluster, CoxII (coxII), and spore coat protein CoxII (coxII) genes, complete cds
1395	11270	21126	1.91	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitor factor (MIF) gene, 5' flanking region and partial cds
1395	11270	21126	1.91	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitor factor (MIF) gene, 5' flanking region and partial cds
1620	11815	21694	0.95	2.1E-02	AF160899.1	NT	Regia auriculata major acetabular protein precursor (TMAP) mRNA, complete cds
2795	10653	20550	3.98	2.1E-02	N92666.1	EST_HUMAN	ye4807 r1 Soerae metazoan 28S rRNA Homo sapiens cDNA clone IMAGE224541 5'
3110	11883	21776	0.85	2.1E-02	BE072546.1	EST_HUMAN	P02-B10546-120100-001-111 B10548 Homo sapiens cDNA
3110	11883	21777	0.85	2.1E-02	AA461271.1	EST_HUMAN	P02-B10546-120100-001-111 B10548 Homo sapiens cDNA
3535	13451	23247	1.23	2.1E-02	AA461271.1	NT	S cerevisiae chromosome IV reading frame ORF YOL245c
4038	13541	23719	0.99	2.1E-02	U74934.1	NT	Borrelia burgdorferi plasmid osp22, ospC and ospD genes, complete cds; and unknown genes
4342	14259	24022	1.61	2.1E-02	AF176814.1	NT	wp81411 x1 Soerae, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE2371509 5'
4351	14247	24033	1.03	2.1E-02	AF176814.1	EST_HUMAN	wp81411 x1 Soerae, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE2371509 5'
4611	14499	24289	4.95	2.1E-02	Y08501.1	NT	A. thaliana mitochondrial genome, part A
4714	14600	24385	0.95	2.1E-02	AB23432.1	NT	wh54953 x1 NCI_CGAP_Kd11 Homo sapiens cDNA clone IMAGE2384628 3'
7533	17404	27618	1.8	2.1E-02	AJ263213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
7533	17404	27619	1.8	2.1E-02	AJ263213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9449	15055		4.99	2.1E-02	Y16213.1	NT	Homo sapiens putative p16 ^{ink4a} pseudogene for hair keratin, exons 2 to 7
9857	16348	25184	3.33	2.1E-02	AF153913.1	NT	Acropallium brachyura major outer membrane protein OmsA precursor (omsA) gene, complete cds
17	10004	19795	1.95	2.0E-02	BF02932.1	EST_HUMAN	165108 x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE330998 3' similar to complete MER1.3
18	10005	19795	7.96	2.0E-02	AW55655.1	EST_HUMAN	QV4-NM0039-27040-187-H05 NN0039 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
239	10225	20040	2.03	2.0E-02	6759353	NT	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
232	10256	20077	2.62	2.0E-02	AA49538.1	EST_HUMAN	act15b10r1 Score: 1114686.0, ST Homo sapiens cDNA clone IMAGE:813307 5'
781	10711	20550	1.75	2.0E-02	6759353	EST	Mus musculus DnB homolog 1 (E. coli) (DnB1), mRNA
1071	10987	20830	0.97	2.0E-02	AL064605.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 (p36.33) of Homo sapiens
1191	11062	20638	1.01	2.0E-02	8622397	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1191	11062	20638	1.01	2.0E-02	8622397	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1330	11727	21600	2.31	2.0E-02	8622458	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1330	11727	21601	2.31	2.0E-02	8622458	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2768	12630		1.75	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3040	10004	19795	1.96	2.0E-02	BF02632.1	EST_HUMAN	7d51c0a.r1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:330968 3' similar to contains MER113 MER1 repetitive element
3106	13051		1.16	2.0E-02	7306474	NT	Mus musculus semo domain, transmembrane domain (TM), end cytoplasmic domain, (seraphorn) B9 (Seraphin), mRNA
3106	13174		3.33	2.0E-02	AF095968.1	NT	Arabidopsis thaliana C2H2 zinc finger protein P2E mRNA, complete cds
3926	13834	23814	1.5	2.0E-02	MF05065.1	NT	P. vulgaris hydroxypoline-rich glycoprotein (HRGP) cDNA, 3' end
5079	14949	24725	0.96	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C103
5085	14955	24730	0.99	2.0E-02	AA466098.1	EST_HUMAN	act15b10r1 Score: 1114686.0, ST Homo sapiens cDNA clone IMAGE:813307 5'
7678	17526		1.8	2.0E-02	U70008.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
7690	17780	28019	1.96	2.0E-02	AB040342.1	EST_HUMAN	7d51c0a.r1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2289516 3'
8377	17929	28176	2.01	2.0E-02	D88184.1	NT	Myobacterium tuberculosis H37Rv complete genome, segment 63102
8978	18566	28849	2.55	2.0E-02	D88184.1	NT	Equus caballus DNA for 17245-hydroxylase/17245-ase, complete cds
8931	18736	29031	3.09	2.0E-02	10947059	NT	Homo sapiens arylkin 3, node of Ranvier (arlyn3) (ANK3), transcript variant 1, mRNA
8931	18736	29032	3.09	2.0E-02	10947059	NT	Homo sapiens arylkin 3, node of Ranvier (arlyn3) (ANK3), transcript variant 1, mRNA
9019	14655	24730	1.41	2.0E-02	AA466098.1	EST_HUMAN	act15b10r1 Score: 1114686.0, ST Homo sapiens cDNA clone IMAGE:813307 5'
9431	12630		1.96	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9628	16536		1.72	2.0E-02	BE169595.1	EST_HUMAN	6014781891 NIH_MGC_B9 Homo sapiens cDNA clone IMAGE:3881477 5'
9628	16536		1.72	2.0E-02	BE169595.1	EST_HUMAN	y404369r1 Score: 1114686.0, ST Homo sapiens cDNA clone IMAGE:24675 5'
9635	18404		4.08	2.0E-02	T80037.1	EST_HUMAN	act15b10r1 Score: 1114686.0, ST Homo sapiens cDNA clone IMAGE:813307 5'
978	10011	20432	1.08	1.9E-02	AA572764.1	EST_HUMAN	act15b10r1 Score: 1114686.0, ST Homo sapiens cDNA clone IMAGE:24675 5'
1599	11904	21984	0.84	1.9E-02	PI18493	SWISSPROT	Empty SPRAGLES HOMEOTIC PROTEIN
1993	11897	21776	2.92	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1993	11897	21780	2.97	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2468	12335	22290	0.97	1.9E-02	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2875	12802	22695	7.08	1.0E-02	AA713856.1	EST_HUMAN	W44065.x1 NCI_QGAP_S51 Homo sapiens cDNA clone IMAGE:128337 3'
2923	12850	22650	1.83	1.0E-02	AV646656.1	EST_HUMAN	AV646656 GLC Homo sapiens cDNA clone GLCBLH07 3'
3222	13146	22650	0.82	1.0E-02	AB03911.1	NT	Utrichinus laevis mitochondrial gene for cytochrome b, complete cds
3390	13174		1.25	1.0E-02	N32350.1	EST_HUMAN	Y28302.s1 Soares, multiple, solidstate 2NH-HSP Homo sapiens cDNA clone IMAGE:284331 3'
3844	13558		5.75	1.0E-02	BE79358.1	EST_HUMAN	601572632.F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:383564 5'
3954	13569	23355	0.98	1.0E-02	AB01183.1	EST_HUMAN	q0407.x1 NCI_QGAP_Lu5 Homo sapiens cDNA clone IMAGE:189720 3' similar to contains Alu repetitive element
3991	13669	23646	1.14	1.0E-02	AF11940.1	NT	Myoclema infans VlnA1 precursor (VlnA1) and VlnA2 precursor (VlnA2) genes, partial cds
4098	13693	23777	1.47	1.0E-02	P09381	SWISSPROT	HOMEOIC BICOID PROTEIN (PRD-4)
4098	13693	23778	1.47	1.0E-02	P09381	SWISSPROT	HOMEOIC BICOID PROTEIN (PRD-4)
4441	14335	24125	2.51	1.0E-02	AL62398.1	EST_HUMAN	W44065.x1 Soares, NSF, F8, 9W, OT, PA, P_31 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element
4844	12356	22220	1.91	1.0E-02	AL10150.2	NT	Myoblasts (H4IIE) DNA chromosome 4, coding fragment No. 50
6398	16778	25108	1.28	1.0E-02	U74712.1	NT	Myoblasts (H4IIE) DNA chromosome 2 (PON2) mRNA, complete cds
6985	16882		1.28	1.0E-02	AL10274.2	NT	Myoblasts (H4IIE) DNA chromosome 4, coding fragment No. 50
7377	17248	27422	1.47	1.0E-02	AF13175.1	EST_HUMAN	601860130.F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:412543 5'
7777	17627	27956	1.31	1.0E-02	BF05832.1	EST_HUMAN	601860130.F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:407925 5'
8294	19516	25137	2.55	1.0E-02	AF101065.1	NT	HindIII-mediated intermediate fragment glen mRNA, complete cds
343	10302	20117	1.44	1.0E-02	AW771104.1	EST_HUMAN	h42506.x1 NCI_QGAP_C017 Homo sapiens cDNA clone IMAGE:302724 3' similar to contains element
670	10604	20421	1.34	1.0E-02	BF03812.1	EST_HUMAN	MER29 repetitive element
1141	11057	20000	1.34	1.0E-02	X17864.1	NT	H1fractin mRNA for myelin basic protein (MBP)
1471	11323	21187	1.23	1.0E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encode (enc) mRNA, complete cds
2845	12512	22403	1.51	1.0E-02	AF04344.1	NT	Proscapha melanogaster cytoplasmic protein encode (enc) mRNA, complete cds
3174	13069		0.89	1.0E-02	AL005529.1	EST_HUMAN	h42506.x1 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:200295 3'
3812	13724	23513	1.09	1.0E-02	AF197122.1	EST_HUMAN	MRI-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3812	13724	23514	1.09	1.0E-02	AF197122.1	EST_HUMAN	MRI-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3998	13903		1.15	1.0E-02	AA891446.1	EST_HUMAN	h42506.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1406593 3'
4332	14228	24011	1.44	1.0E-02	AF193683.1	SWISSPROT	HYPOPHYSAL PROTEIN D184502.2
4737	14753	24832	1.05	1.0E-02	D06310	EST_HUMAN	HYPOPHYSAL PROTEIN D184502.2
4897	14767	24543	1.05	1.0E-02	U28670.1	EST_HUMAN	HYPOPHYSAL PROTEIN D184502.2
6075	16058	26207	3.95	1.0E-02	P14310	SWISSPROT	HYPOPHYSAL PROTEIN D184502.2
7500	17411		2.49	1.0E-02	AA897543.1	EST_HUMAN	h42506.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1364621 3' similar to gbl.11672 ZINC FINGER PROTEIN 91 (HUMAN)

Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF REQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7780	17640	27873	1.51	1.E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:380985 5'
7871	17721	27950	1.23	1.E-02	XG6933.1	NT	Ligase III mRNA for myomodulin/neuropeptide precursor
8795	17864	28126	1.78	1.E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8795	17864	28127	1.78	1.E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
8896	18697	28991	1.76	1.E-02	AF000006.1	NT	Proxocara boviculifl OT3 genome DNA, 165001-148500 nt, position (67)
8912	18706	29000	3.12	1.E-02	U62749.1	NT	Zammya acid (Bommal protein P2a3 (m29a3) mRNA, partial cds
8912	18486		1.29	1.E-02	AF047475.1	EST_HUMAN	Drosophila melanogaster protein (proctid) gene, partial cds
888	10814	20682	1.29	1.E-02	BE384669.1	EST_HUMAN	60137026F1 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:383210 5'
			1.29	1.E-02	AF047475.1	EST_HUMAN	1.E11 L1 repetitive element
			2.24	1.E-02	AW57183.1	EST_HUMAN	hH4403.x1 Soares_NFL1_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains 1.E11 L1 repetitive element
1750	11650	21519	2.24	1.E-02	AW57183.1	EST_HUMAN	hH4403.x1 Soares_NFL1_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains 1.E11 L1 repetitive element
1750	11650	21520	2.24	1.E-02	AW57183.1	EST_HUMAN	hH4403.x1 Soares_NFL1_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains 1.E11 L1 repetitive element
1828	11725		3.08	1.E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment H821C004
2065	11656		13.03	1.E-02	AB04316.1	NT	Oryzavirus cuniculus mRNA for mitogen-activated protein kinase (RABEX3) mRNA
2063	12471		1.35	1.E-02	7857465	NT	Homo sapiens putative Rab5 GTP/GTP exchange factor homologous (RABEX3) mRNA
2668	12695	22595	0.92	1.E-02	AI147615.1	EST_HUMAN	q622068.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:195862 3'
			4.17	1.E-02	AV182768.1	EST_HUMAN	hH4504.x1 NC1_GCAP_RDP1 Homo sapiens cDNA clone IMAGE:301533 3' similar to contains MER18.b1 MER19 repetitive element
3467	13353		0.88	1.E-02	PQ4029	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3673	13487		0.98	1.E-02	AG080418.1	EST_HUMAN	cd1904.x1 Strigamia ovary (8937217) Homo sapiens cDNA clone IMAGE:56927 3' similar to contains Alu repetitive element/contains element MER2A repetitive element
4078	13980		1.78	1.E-02	R02506.1	EST_HUMAN	y65108.x1 Soares_fetal liver spleen INF.S1 Homo sapiens cDNA clone IMAGE:124947 5'
4105	14005		1.24	1.E-02	AW57183.1	EST_HUMAN	hH4403.x1 Soares_NFL1_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains 1.E11 L1 repetitive element
4427	14322	24109	1.77	1.E-02	U00641.1	NT	Messenger RNA for angiotensin (Lopholaima americanus) somatostatin II
4615	14363	24291	5.27	1.E-02	N018073.1	EST_HUMAN	cd16102.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:164065 3'
4708	14394		5.47	1.E-02	AF105973.1	NT	Murid herpesvirus 4 complete genome
4937	14942	24612	1.53	1.E-02	AT69247.1	EST_HUMAN	w83803.x1 Soares_NSF_F8_9M_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2957113 3' similar to contains Alu repetitive element
5726	15632	25735	1.81	1.E-02	U196247.1	EST_HUMAN	Homo sapiens nebulin (NEB) mRNA
6276	16140	26266	1.31	1.E-02	AJ007170.1	NT	Homo sapiens hypoxan gene, exon 1-50
6554	16412		1.48	1.E-02	AL04054.1	EST_HUMAN	DFZ234303.11.T1.434 (synonym: hsc3) Homo sapiens cDNA clone DFZ234303.14 5'
7692	17443	27656	2.25	1.E-02	AW50482.1	EST_HUMAN	Q14L.NH1030.04040-130-106 (NH1030) Homo sapiens cDNA
9761	19693		1.96	1.E-02	Q65271	SWISSPROT	P15TL.SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)
9861	19362		1.96	1.E-02	Q65271	SWISSPROT	P15TL.SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF BEQ ID NO.	Expression Signal ID NO.	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
501	10443		1.38	1.6E-02	AL021823.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162
1695	11539	21399	1.13	1.6E-02	U19890.1	NT	Tropicam multiphilum flb2, flb3 and flbD genes for flagellin subunit proteins and CAP protein homologue
2202	12069	21900	1.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (ECASYN) (ESTERASE-22)
2302	12069	21961	1.13	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (ECASYN) (ESTERASE-22)
2518	12362	22284	0.98	1.6E-02	AJ003345.1	NT	Homo sapiens KLOT1 gene
2656	12474	22886	1.47	1.6E-02	AJ444672.1	EST_HUMAN	ncs1-06a1 NCI CGAP Exrt Homo sapiens cDNA clone IMAGE:510697
2662	12529		1.74	1.6E-02	AB014834.1	NT	Homo sapiens mRNA for KIA0834 protein, partial cds
3481	13397	23202	3.83	1.6E-02	AW80052.1	EST_HUMAN	U3-070219-16020-065-007 CT0219 Homo sapiens cDNA
4084	13686		2.16	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NC28, RPS28, NADH cytochrome oxidase, NG28, KFC1, Fas-binding protein, BING1, Iqbalin, FasLQDS-like, KE2, BING4, beta 1, 3-galactosyl transferase, and RPS18 genes, complete cds; Saccaromyces cerevisiae gene, partial cds
4203	14102	23596	0.94	1.6E-02	AV875407.1	EST_HUMAN	QV22P10072-140100-030-007 P10072 Homo sapiens cDNA
5450	15377	25437	1.31	1.6E-02	AL161908.2	NT	Mus musculus CDS antigen (C26), mRNA
6003	15009	26232	2.11	1.6E-02	AB015281.1	NT	Candida albicans CAG033 gene, complete cds
6758	16037		4.01	1.6E-02	U05151.1	NT	Human apoc-II gene for pre-apolipoprotein C-II
7773	17523		2.71	1.6E-02	AF078784.1	NT	Drosophila melanogaster enhancer of polycomb (Epc) mRNA, complete cds
7954	17804	28044	1.47	1.6E-02	AA572918.1	EST_HUMAN	ntf19g03.at NCI CGAP_P41 Homo sapiens cDNA clone IMAGE:914290 similar to SW:TELO_P48B1
7954	17804	28045	1.47	1.6E-02	AA572918.1	EST_HUMAN	P29294 TELOKIN (1):
8260	19473	28401	2.17	1.6E-02	U34628.1	NT	G gallus microsatellite DNA (LEI026) (c-TTGGTCTT)
8544	18416	26883	2.52	1.6E-02	AL161908.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8544	18416	26884	2.52	1.6E-02	AL161908.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8501	18915	26905	1.91	1.6E-02	AJ373558.1	EST_HUMAN	q95801.Xt Soares, pregnant, uterus, NH-P41 Homo sapiens cDNA clone IMAGE:201242.3
9211	12069	21900	1.35	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (ECASYN) (ESTERASE-22)
9211	12069	21961	1.35	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (ECASYN) (ESTERASE-22)
9679	19155		2.3	1.6E-02	X62751.1	NT	R. norvegicus gene for cholera toxin subunit, exon 1 (non coding)
9679	19155		1.42	1.6E-02	U1417899	NT	Homo sapiens SEC14 (S. cerevisiae) like 2 (SEC14L2), mRNA
9794	10066	7934	2.61	1.6E-02	B023744	NT	Homo sapiens transcription factor (HSA130859), mRNA
2065	11694	21979	3.81	1.5E-02	U36824.1	EST_HUMAN	X42767.at Soares fetal liver spleen 1N1S Homo sapiens cDNA clone IMAGE:249325.3
2128	12016	21914	2.38	1.5E-02	AL161908.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
3023	12551	22743	1.44	1.5E-02	AJ006216.1	NT	Homo sapiens CAGNA1F gene, exons 1 to 48
3023	12551	22744	1.44	1.5E-02	AJ006216.1	NT	Homo sapiens CAGNA1F gene, exons 1 to 48

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3683	13577	23365	0.9	1.E-02/BF02642.1	EST_HUMAN	EST_HUMAN	MR4-TN015-080600-201-617 TN016 Homo sapiens cDNA
4049	13351	23727	1.23	1.E-02/AA100025.1	EST_HUMAN	EST_HUMAN	z40410.1 Stage18 INT neuron (6557233) Homo sapiens cDNA clone IMAGE:63228 5'
4967	14293	24048	0.81	1.E-02/AF260225.1	NT	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5801	15707	25819	1.91	1.E-02/Q09711	SWISSPROT	SWISSPROT	HYPOPHARYNGEAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
6301	16150	26197	1.66	1.E-02	11467282	NT	Cytoplasmic peroxisome cytochrome c, complete genome
6377	16236	26399	1.36	1.E-02	11467282	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
6596	16476	26580	1.33	1.E-02/AL163303.2	NT	NT	Homo sapiens chromosome 21 segment HS2CTC103
6600	16490	26580	3.44	1.E-02	11417739	NT	Homo sapiens chromosome 21 segment HS2CTC103
7126	17003	27195	1.23	1.E-02/BF345584.1	EST_HUMAN	EST_HUMAN	602018135F1 INT CGAP_Bln67 Homo sapiens cDNA clone IMAGE:3754504 5'
7520	17339	27545	2.07	1.E-02/D44006.1	NT	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
7646	17466	27717	1.25	1.E-02/R32667.1	EST_HUMAN	EST_HUMAN	MF4210.1 Soares placenta N23HP Homo sapiens cDNA clone IMAGE:133531 5'
7648	17466	27718	1.25	1.E-02/R32667.1	EST_HUMAN	EST_HUMAN	MF4210.1 Soares placenta N23HP Homo sapiens cDNA clone IMAGE:133531 5'
8508	18330	29847	2.5	1.E-02/L40009.1	NT	NT	Plasmodium falciparum (strain FC3) variant-specific surface protein (var-2, var-3) genes, complete cds
8428	19559		1.32	1.E-02/AW150834.1	EST_HUMAN	EST_HUMAN	RC4-CCN0049-140102-011-011 CN049 Homo sapiens cDNA
5680	19437		1.47	1.E-02/AL14130.1	EST_HUMAN	EST_HUMAN	AL134750 PLAGE1 Homo sapiens cDNA clone IMAGE:1008374 5'
411	10337		1.45	1.E-02/AF02230.2	NT	NT	Chromoglycin precursor AR33, section 53 of 94 of the complete genome
1102	11018	20880	3.99	1.E-02/7705880	NT	NT	Homo sapiens NESH1 protein (LOC51225), mRNA
1296	11183		1.35	1.E-02/U32900.1	NT	NT	Hemophilus influenzae Rd section 115 of 163 of the complete genome
1276	11184		2.02	1.E-02/U67761.1	NT	NT	Xenopus laevis neurogranin related 1b (XN-NGR-1b) mRNA, complete cds
1374	11280		0.84	1.E-02/AJ216854.1	EST_HUMAN	EST_HUMAN	Homo sapiens headpin gene, complete cds
1501	11405		0.80	1.E-02/AV727585.1	EST_HUMAN	EST_HUMAN	AV727585 H1B Homo sapiens cDNA clone HTB4-H11 5'
3176	13101	22805	1.9	1.E-02/AF160880.2	NT	NT	Bifidobacterium longum NeriH+ antiporter (rhuf), cytosine deaminase, and alpha-galactosidase (egl) genes, complete cds; and N-acetylglucosaminylxylase repressor protein (tagC2xR) gene, partial cds
3352	13272	23074	0.89	1.E-02/AV074212.1	EST_HUMAN	EST_HUMAN	z005409.x1 INT CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2575763 3'
3439	13356	23161	5.21	1.E-02/AL161589.2	NT	NT	Arabidopsis thaliana DNA chromosome 4, contig Fragment No. 82
3439	13356	23162	5.21	1.E-02/AL161589.2	NT	NT	Arabidopsis thaliana DNA chromosome 4, contig Fragment No. 82
3476	13392	23197	0.88	1.E-02/4603628	NT	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
3606	13520	23308	8.16	1.E-02/6946919	NT	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4337	14293	24042	7.26	1.E-02/AW962988.1	EST_HUMAN	EST_HUMAN	EST1374761 MAGE resequences, MAGEG Homo sapiens cDNA
4337	14293	24043	7.26	1.E-02/AW962988.1	EST_HUMAN	EST_HUMAN	EST1374761 MAGE resequences, MAGEG Homo sapiens cDNA
4175	14659	24445	6.7	1.E-02/BE7133142.1	EST_HUMAN	EST_HUMAN	601567/AG0371 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
4175	14659	24446	6.7	1.E-02/BE7133142.1	EST_HUMAN	EST_HUMAN	601567/AG0371 NH1_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5602	15768	25887	4.92	1.4E-02	AA559030.1	EST_HUMAN	nt1c04.s1 NCI_OGAP_Bi2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
5602	15768	25888	4.92	1.4E-02	AA559030.1	EST_HUMAN	nt1c04.s1 NCI_OGAP_Bi2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
5922	16612	25888	4.92	1.4E-02	AL022073.1	NT	Myocardial tuberculin H57Nv complete genome; segment 88/102
7408	17275	27481	2.07	1.4E-02	BE544591.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3446241 5'
9126	19885	28790	4.78	1.4E-02	X60459.1	NT	Human FNAR gene for interferon alpha/beta receptor
9478	19102		1.95	1.4E-02	AF324693.1	NT	Arabidopsis thaliana P21J9.2 mRNA, complete cds
9733	19277		1.96	1.4E-02	11420693	NT	Homo sapiens sperm associated antigen 7 (SPAC7), mRNA
1621	11768	21684	0.96	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:382835 5'
1672	11907		2.41	1.3E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C001
3177	13102	22936	1.66	1.3E-02	BF627091.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3177	13102	22907	1.89	1.3E-02	BF627091.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3888	13789		1.41	1.3E-02	AF166288.1	NT	Mus musculus beta-actin/cytokeratin gene, complete cds
5176	11807	21684	1	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5212	15135	24854	1.36	1.3E-02	AL046988.2	NT	Mus musculus chromosome X contig; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, imxqzsf1
5212	15135	24855	1.36	1.3E-02	AL046988.2	NT	Mus musculus chromosome X contig; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, imxqzsf1
6156	15114	24856	1.35	1.3E-02	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6156	15114	24857	1.35	1.3E-02	AL161548.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
6473	16392	26496	4.77	1.3E-02	AD31593.1	EST_HUMAN	ov0605.x1 Soares, parathyroid tumor, NciPFA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element
6039	16817	27010	1.74	1.3E-02	AF15991.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
7682	17712	27956	1.97	1.3E-02	M83707.1	EST_HUMAN	Mouse kidney androgen-regulated protein (KARP) gene, complete cds
8390	18237	28484	4.39	1.3E-02	AW26893.1	NT	xx04403.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'
8390	18237	28485	4.39	1.3E-02	AW26893.1	EST_HUMAN	xx04403.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815038 3'
9102	19705		2.92	1.3E-02	X31780.1	NT	Yeast ABP1 gene for actin binding protein
9432	19864		1.6	1.3E-02	Z59117.1	NT	Bacillus subtilis complete genome (section 14 of 21) from Z591451 to Z591470
9536	19710		1.8	1.3E-02	9633069	NT	Human herpesvirus B3, complete genome
9798	19485		28.84	1.3E-02	AF16238.1	NT	Homo sapiens Y1b vasopressin receptor (VPR3) gene, complete cds
9849	19744	24672	1.32	1.3E-02	AF009178.1	NT	Oryza sativa replication protein A1 (Oa-RepA1) mRNA, complete cds
205	10177		0.94	1.2E-02	Z87544.1	NT	H.sapiens DMA, DM1, HLA-Z1, IIP2, LIMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING3, 9, 13 and 14 genes

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
302	10310	20128	1.74	1.2E-02	AA085909.1	EST_HUMAN	zif501.1 Scores: refina N2b-HR Homo sapiens cDNA clone IMAGE:381940 3' similar to contains element L1 repetitive element ;
445	10399	20210	1.48	1.2E-02	P38596	SWISSPROT	HYPOPHARYNGEAL 171 KD PROTEIN IN PUG3 REGION qf80a.2.x1 Scores: testis_NHT Homo sapiens cDNA clone IMAGE:174670 3' similar to contains L1.11 L1 repetitive element ;
721	10653	20483	2.88	1.2E-02	AI18522.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS27C13
2130	12018	21916	1.95	1.2E-02	AI163213.2	NT	X67609.x1 Scores: NFL_T_GBC 31 Homo sapiens cDNA clone IMAGE:2659432 3'
2393	12271	22167	1.26	1.2E-02	AW172950.1	EST_HUMAN	X67609.x1 Scores: NFL_T_GBC 31 Homo sapiens cDNA clone IMAGE:3454008 5'
2448	12325	22223	1.1	1.2E-02	BE598310.1	EST_HUMAN	607038-006F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454008 5'
2448	12325	22224	1.1	1.2E-02	BE598310.1	EST_HUMAN	607038-006F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454008 5'
2598	12271	22167	1.27	1.2E-02	AW172950.1	EST_HUMAN	X67609.x1 Scores: NFL_T_GBC 31 Homo sapiens cDNA clone IMAGE:2659432 3'
3003	12600		6.16	1.2E-02	AA076418.1	EST_HUMAN	zif501.1 Scores: refina N2b-HR Homo sapiens cDNA clone IMAGE:345020 5'
3230	13173	22371	1.95	1.2E-02	R62956.1	EST_HUMAN	yf11068.s1 Scores: placenta N2b4P Homo sapiens cDNA clone IMAGE:138603 3'
4890	14712	24495	2.04	1.2E-02	U9128.1	NT	Human heterodimeric haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rofa gene, and solid phosphate transporter (NPT3) gene, complete cds
4874	14849		1.73	1.2E-02	AB019786.1	NT	Cytosolic pyrophosphatase GpUBAT mRNA, partial cds
5017	14861	24856	2.12	1.2E-02	AV757104.1	EST_HUMAN	AT73104 HIT Homo sapiens cDNA clone HTFBC0311 5'
8516	15434	25497	1.96	1.2E-02	D78966.1	NT	Rana rugosa mRNA for calreticulin, complete cds
6180	10060	20216	5.93	1.2E-02	AF176412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
6327	16190	20352	6.37	1.2E-02	AV720653.1	EST_HUMAN	AT732083 HIT Homo sapiens cDNA clone HTFBC0311 5'
6695	16545	20742	2.11	1.2E-02	Q11205	SWISSPROT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAc09) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL.2) (SIA74B)
6785	16644	20832	1.22	1.2E-02	AF169612.1	NT	Homo sapiens fringe protein mRNA, partial cds
6785	16644	20833	1.22	1.2E-02	AF169612.1	NT	Homo sapiens fringe protein mRNA, partial cds
7102	17029		1.17	1.2E-02	T76867.1	EST_HUMAN	yf72008.s1 Scores: fetal liver spleen NFLS Homo sapiens cDNA clone IMAGE:113774 3'
7557	17403	27923	2.45	1.2E-02	AB031013.1	NT	Novwalk-like virus group 2 gene for capsid protein, complete cds
7576	17403	27640	1.73	1.2E-02	AJ246003.1	NT	Homo sapiens Spst gene for spastin protein
9177	18618	28345	1.78	1.2E-02	O15934	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU) (HPER)
6688	19575		1.5	1.2E-02	Q18119.1	EST_HUMAN	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
6798	10266		3.47	1.2E-02	CA070564.1	EST_HUMAN	CB1819 Human placenta cDNA (Tf91wra) Homo sapiens cDNA clone GEN-557006 5'
1248	11165	21004	1.32	1.1E-02	CA070564.1	EST_HUMAN	zif501.1.s1 Stratiogene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:550924 3'
1679	11881	21461	1.99	1.1E-02	XT75491.1	NT	H.sapiens LIPA gene, exon 4
1679	11881	21462	1.99	1.1E-02	XT75491.1	NT	H.sapiens LIPA gene, exon 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1992	11886	21178	4.35	1.E-02	BF345293.1	EST_HUMAN	00207160371 INCL_CGAP_Bin67 Homo sapiens cDNA clone IMAGE:415808 5'
2848	12776		3.33	1.E-02	N99523.1	EST_HUMAN	zkl04051T Homo sapiens liver spleen INFLS Homo sapiens cDNA clone IMAGE:359040 5'
2933	12850	22560	10.39	1.E-02	AF050065.1	NT	Homo sapiens MHC class I region
3478	13394	23200	2.46	1.E-02	AB53508.1	EST_HUMAN	qp5010.x1 INCL_CGAP_OV23 Homo sapiens cDNA clone IMAGE:221639 3' similar to SW_XPF_HUMAN
3937	13846		0.97	1.E-02	BE114637.1	EST_HUMAN	Q02889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4016	13921		0.97	1.E-02	AW13766.1	EST_HUMAN	RC3-S10197-120200-016-011 S10197 Homo sapiens cDNA
4728	14609	24395	1.51	1.E-02	AL048383.2	EST_HUMAN	DKFZ598E0924_s1 598 (Synonym: Iutein) Homo sapiens cDNA
4821	14704		0.92	1.E-02	AW120281.1	EST_HUMAN	OV2-S10296-150200-028-011 S10296 Homo sapiens cDNA
6490	16539	26506	2.36	1.E-02	BE106811.1	EST_HUMAN	RC1-H10256-100300-016-007 H10256 Homo sapiens cDNA
7100	17037	27230	6.97	1.E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
7710	17580	27785	2.25	1.E-02	AA02578.1	EST_HUMAN	z02400.L1 Striatogene neuroepithelium NT2RA/AV1 687284 Homo sapiens cDNA clone IMAGE:548328 5'
7810	17660	27900	4.11	1.E-02	AA31465.1	EST_HUMAN	EST_186242 Colon carcinoma (HCC) cell line H1 Homo sapiens cDNA 5' end
8347	18224	28476	3.38	1.E-02	11436903	NT	Homo sapiens T-box 5 (TBX5), mRNA
8094	18845		2.23	1.E-02	AA68296.1	EST_HUMAN	id07711.L1 Striatogene fetal retina 637202 Homo sapiens cDNA clone IMAGE:653005 3' similar to contains
6	9962	19785	3.35	1.E-02	AA68296.1	EST_HUMAN	All repetitive elements
1505	11411	21270	0.81	1.E-02	AW368128.1	EST_HUMAN	MPS-CT10175-11088-003-410 CT10175 Homo sapiens cDNA
2526	12899		1.2	1.E-02	AA306188.1	EST_HUMAN	CM2-H10177-047086-07412 H10177 Homo sapiens cDNA
3051	12978	22771	2.37	1.E-02	BE835556.1	EST_HUMAN	cc22006.at INCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:130046 3'
3226	13150	22950	1.18	1.E-02	BE835556.1	EST_HUMAN	RC3-N0025-250300-021-402 FN0025 Homo sapiens cDNA
3464	13380		0.99	1.E-02	AA146221.1	EST_HUMAN	G0149826F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:363396 3'
3805	13717	23505	0.79	1.E-02	AA05036.1	EST_HUMAN	MRO-CT0069-081096-003-R10 CT0060 Homo sapiens cDNA
4697	14553	24345	4.26	1.E-02	6753521	NT	H00821 Human fetal liver cDNA library Homo sapiens cDNA
4736	14621	24407	2.38	1.E-02	R06957.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4965	15016	24653	0.85	1.E-02	AF1218610.1	NT	y05401T1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:196035 5'
5149	15016		2.74	1.E-02	AV1577113.1	EST_HUMAN	Homo sapiens atrial precursor (A1RN) gene, exon 26 and complete cds, alternatively spliced
5761	15659	25767	2.74	1.E-02	BE87639.1	EST_HUMAN	G0149826F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:363396 5'
6054	16337	26178	2.06	1.E-02	Z0942.1	NT	MR4-B10395-070100-201-H01 BT0356 Homo sapiens cDNA
7403	17270	27476	4.95	1.E-02	BF036331.1	EST_HUMAN	Z.maya UsbRNA pseudogene
7403	17270	27476	4.95	1.E-02	BF036331.1	EST_HUMAN	G01495070F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:363377 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (CpG) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8586	18454		2.1	1.0E-02	AF167659.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds, mitochondrial gene for mitochondrial product
8574	19552	28846	2.03	1.0E-02	AV760016.1	EST_HUMAN	AV760016 MDS Homo sapiens cDNA clone MDSBDC16 5'
8142	19762		1.7	1.0E-02	Q82203	SWISSPROT	SPLICING FACTOR 3A SUBUNIT 2 (SF3A60)
8222	19535	25061	2.95	1.0E-02	AW693521.1	EST_HUMAN	RC2D70007-120200-07H402 DT0007 Homo sapiens cDNA
8217	19560		5.22	1.0E-02	S70300.1	NT	Homo sapiens renal lipoprotein (RDP) gene, complete cds
8745	19845		2.44	1.0E-02	X62054.1	NT	H. sapiens gene for Mx19/10503 antigen
876	10801		1.7	9.0E-03	AI798126.1	EST_HUMAN	WH2309.x1 NCL CGAP_K4111 Homo sapiens cDNA clone IMAGE:2389433 3' similar to contains element
1243	11150	20951	1.97	9.0E-03	BE718683.1	EST_HUMAN	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2346	12226	22123	3.36	9.0E-03	AL161599.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2563	12463	22345	1.08	9.0E-03	A246727.1	NT	Oncorhynchus nerka proviral gypsy/retroviruses partial reverse transcriptase and protease genes (pol genes)
2563	12463	22346	1.08	9.0E-03	A246727.1	NT	Oncorhynchus nerka proviral gypsy/retroviruses partial reverse transcriptase and protease genes (pol genes)
2876	12803	22597	0.83	9.0E-03	AI261744.1	EST_HUMAN	950009.x1 Soverc_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:184281 3'
2876	12803	22598	0.83	9.0E-03	AI261744.1	EST_HUMAN	950009.x1 Soverc_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:184281 3'
3817	13331	23317	0.92	9.0E-03	U05184.1	NT	S. dubautii-like Brucella genes, complete cds
4814	14753	24568	1.17	9.0E-03	BE017946.1	EST_HUMAN	1244610.Y1 NCL CGAP_Sm22 Homo sapiens cDNA clone IMAGE:2291466 5'
5181	15045		2.56	9.0E-03	AF117240.1	NT	S. argemont sp. mixed lineage leukemia-like protein (ML) gene, partial cds
5697	15902		4.17	9.0E-03	BE718683.1	EST_HUMAN	601673438F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3534752 3'
6897	16477		1.18	9.0E-03	AL038991.1	EST_HUMAN	DNK74944.0412.11 431 (synonym: hae3) Homo sapiens cDNA clone DNK74944.0412 5'
7673	17623	27748	1.47	9.0E-03	P20306	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
8354	18231		1.95	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
9352	19763		1.34	9.0E-03	BF351141.1	EST_HUMAN	PMH-HT0462-287299-001-403 HT0462 Homo sapiens cDNA
9557	19763		1.59	9.0E-03	BE348385.1	EST_HUMAN	hw17605.x1 NCL CGAP_Lux2 Homo sapiens cDNA clone IMAGE:3183101 3'
9552	19545		1.27	9.0E-03	AF137290.1	NT	S. argemont sp. mixed lineage leukemia-like protein (ML) gene, partial cds
9549	19275	26250	1.32	9.0E-03	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
9843	19341		27.84	9.0E-03	BF351141.1	EST_HUMAN	PMH-HT0462-287299-001-403 HT0462 Homo sapiens cDNA
493	10436		3.2	8.0E-03	AA72307.1	EST_HUMAN	zh30c03.x1 Soverc_pinal_gland_N84-PG Homo sapiens cDNA
973	10897	20744	46.2	8.0E-03	AF106656.1	NT	Alu repetitive element
2113	12002	21800	2.38	8.0E-03	AL163283.2	NT	Homo sapiens adenylocuccinate lyase gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HR BLAST E Value	Top HR Accession No.	Top HR Database Source	Top Hit Descriptor
2930	12857		0.86	8.0E-03	AF10748.1	NT	Escherichia coli microtub. 24 region, DNA binding protein (mdaA), immunity protein (mtf), microtub. 24 (mtf),
3270	13161	22590	0.97	8.0E-03	BE171226.1	EST_HUMAN	lent microtub. transport protein (mtfA, mtfB) genes, complete cds
3314	13235	23039	0.89	8.0E-03	AI131016.1	NT	RC1-HT0545-120200-011-569 HT0545 Homo sapiens cDNA
3762	13704		1.07	8.0E-03	AF08764.1	NT	Homo sapiens SCL gene locus
4266	14185	23695	5.12	8.0E-03	BF93327.1	EST_HUMAN	Xenopus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds
							CM4NN0119-300600-223-605 NN0119 Homo sapiens cDNA
							Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, lapasin, RALGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
5391	15310	25164	2.7	8.0E-03	AF110820.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-344000 nt. position (2/7)
5761	19453	25775	1.35	8.0E-03	AF000002.1	NT	PROBABILE PEPTIDASE Y4NA
6048	15051	20081	4.52	8.0E-03	F55577	SWISSPROT	A. californica (marine gastropod mollusc) neurotrophin gene (seq. cell), exon 1, 5' end
6279	16143	28269	2.19	8.0E-03	U11717.1	NT	Turkey trachea mRNA for p40-phox, complete cds
6463	16314		1.86	8.0E-03	AB036267.1	NT	MR1-ST0111-111189-011-066 ST0111 Homo sapiens cDNA
7169	17043	27235	3.91	8.0E-03	AW098262.1	EST_HUMAN	QV1-BT0077-046406-131-c03 BT0077 Homo sapiens cDNA
7717	17567		4.72	8.0E-03	BE049509.1	EST_HUMAN	6147475191F1 NIH MGCC 68 Homo sapiens cDNA, clone IMAGE:3679405.5
8148	18308	28284	1.92	8.0E-03	BF78441.1	EST_HUMAN	Scarsilia chromosoma X coding frame ORF Y18126v
8363	18320		2.78	8.0E-03	Z49824.1	NT	0480403.1 NCI CGAP_O2 Homo sapiens cDNA, clone IMAGE:374232
8697	18575	28565	1.75	8.0E-03	AA82517.1	EST_HUMAN	0480403.1 NCI CGAP_O2 Homo sapiens cDNA, clone IMAGE:374232
8897	18575	28565	1.75	8.0E-03	AA82517.1	EST_HUMAN	Homo sapiens melanoma-associated antigen (IMAGE-C7) gene, complete cds
8983	18760	29053	4.83	8.0E-03	AF04396.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
9075	18852		1.34	8.0E-03	U69035.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
9121	18882		3.36	8.0E-03	AB038161.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
679	10612	20403	11.58	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
679	10612	20404	11.58	7.0E-03	AF097183.1	NT	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
691	10884	20732	2.01	7.0E-03	AF43376.1	NT	AF147121 HTF Homo sapiens cDNA, clone HTFAZ10.5
1100	11016	20658	2.6	7.0E-03	AV731712.1	EST_HUMAN	FORHEAD BOX PROTEIN D3 (HNF1P/TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1341	11247		1.16	7.0E-03	Q81060	SWISSPROT	NUCLEAR FACTOR 3 FORK-HEAD HOMOLOG 2 (HFX-2)
1373	11279	21135	13.73	7.0E-03	AA098268.1	EST_HUMAN	ab79606.1 S1 Stralagene fetal retina 957202 Homo sapiens cDNA, clone IMAGE:383145.3
1466	11391	21251	4.6	7.0E-03	AA035069.1	SWISSPROT	xx21022.x1 Scores. NFL_1 GBC_S1 Homo sapiens cDNA, clone IMAGE:2813739.3
2210	12715	22001	2.24	7.0E-03	Q04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3702	13616	23400	1.27	7.0E-03	AW44463.1	EST_HUMAN	UH-HBB-abb-c-10-U1.1 NCI CGAP_S1 Homo sapiens cDNA, clone IMAGE:2733691.3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3741	13053	25436	1.01	7.0E-03	AF196344.1	NT	Reptus nervigous neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
4434	14328		1.23	7.0E-03	AW117711.1	EST_HUMAN	h34406.x1 NCL CGAP UTI Homo sapiens cDNA clone IMAGE:200903.3 similar to TR-Q12887 Q12887
4495	14359		1.01	7.0E-03	AW60388.1	EST_HUMAN	h34406.x1 NCL CGAP UTI Homo sapiens cDNA clone IMAGE:200903.3 similar to TR-Q12887 Q12887
4016	14765		1.76	7.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS2: C078
6038	14670	24683	1.1	7.0E-03	BE044191.1	EST_HUMAN	h038008.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR-O83434
6038	14670	24684	1.1	7.0E-03	BE044191.1	EST_HUMAN	h038008.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3039807 3' similar to TR-O83434
6717	19452		6.07	7.0E-03	AW661056.1	EST_HUMAN	O03434 RETICULOCALBIN.1
5813	15718	25931	1.49	7.0E-03	W66251.1	EST_HUMAN	FC1-012295-050400-018-c08 GT0283 Homo sapiens cDNA
6039	16544	25937	3.46	7.0E-03	AA327129.1	EST_HUMAN	233310.1 Scores_fetal heart_NH116W Homo sapiens cDNA 5' end
5954	16859	25980	1.3	7.0E-03	BE67395.1	EST_HUMAN	EST300574 Colon 1 Homo sapiens cDNA 5' end
6210	16502	26127	2.39	7.0E-03	BE528133.1	EST_HUMAN	Q734810.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3008347 3' similar to TR-Q13387
8441	16502	25466	4.98	7.0E-03	Z58838.1	NT	Q142-010478-230900-347-011 GT0478 Homo sapiens cDNA
8441	16502	25467	4.98	7.0E-03	Z58838.1	NT	Q142-010478-230900-347-011 GT0478 Homo sapiens cDNA
6723	16603	26732	2.29	7.0E-03	BE176697.1	EST_HUMAN	S cervicatis chromosome II reading frame ORF Y81077w
7603	17450	27070	2.63	7.0E-03	P45982	SWISSPROT	RC6-H10562-160300-011-D02 HT0562 Homo sapiens cDNA
7603	17450	27071	2.63	7.0E-03	P45982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
7603	17450	27071	2.63	7.0E-03	P45982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8201	18086	26337	3.36	7.0E-03	A000662.1	NT	AY032793 GRC Homo sapiens cDNA clone GRCAC01 6
9609	19760		1.65	7.0E-03	HE4065.1	EST_HUMAN	Poa laurus mRNA for NUP-62, complete cds
9615	19164		1.88	7.0E-03	BE26383.1	EST_HUMAN	Y17801.1 Scores_fetal liver spleen INTLS Homo sapiens cDNA clone IMAGE:242693 3' similar to contains
9902	19425		1.83	7.0E-03	AW68810.1	EST_HUMAN	Alu repetitive element
1220	11129	20978	9.29	6.0E-03	AW511148.1	EST_HUMAN	RC1-011451-0472 NHE11MGC_18 Homo sapiens cDNA clone IMAGE:3160476 5'
1220	11129	20980	9.29	6.0E-03	AW511148.1	EST_HUMAN	RC1-011451-0472 NHE11MGC_18 Homo sapiens cDNA clone IMAGE:3160476 5'
2744	12006	22498	1.09	6.0E-03	AF112374.1	EST_HUMAN	h022065.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2962	12790	22581	3.11	6.0E-03	AA789135.1	EST_HUMAN	SW PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR ;
2862	12790	22582	3.11	6.0E-03	AA789135.1	EST_HUMAN	SW PXR_HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXR ;
							Danio rerio odorant receptor gene cluster
							h478611.1 Scores_hisids_NHT Homo sapiens cDNA clone 1321772 3'
							h478611.1 Scores_hisids_NHT Homo sapiens cDNA clone 1321772 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top HE Descriptor
3208	13132		2.06	6.0E-03	H7590.1	EST_HUMAN	y7704.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211351 5'
3264	13187		0.82	6.0E-03	AF160333.1	NT	Nucleoside sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3336	13296	23002	1.24	6.0E-03	U06880.1	NT	Fugu natripase zinc finger protein, isoform, fatty acid binding protein, sepiapterin reductase and vasodilin genes, complete cds
3336	13296	23003	1.24	6.0E-03	U06880.1	NT	Fugu natripase zinc finger protein, isoform, fatty acid binding protein, sepiapterin reductase and vasodilin genes, complete cds
3469	13419		1.05	6.0E-03	W37955.1	EST_HUMAN	z01341.r1 Soares parathyroid tumor, NBHFA Homo sapiens cDNA clone IMAGE:325172 5'
3910	13524	23311	3.62	6.0E-03	BF510596.1	EST_HUMAN	U1H844pm-c9-cu11 x1 NCI CGAP 3u83 Homo sapiens cDNA clone IMAGE:3087754 3'
3711	13624	23407	1.28	6.0E-03	6754023	NT	Mus musculus glucosamine-6-phosphate deaminase (G6p), mRNA
3846	13737	23551	0.93	6.0E-03	A1847884.1	EST_HUMAN	RC3-C10204-240590-02H-B10 C10204 Homo sapiens cDNA
3873	13794		1.18	6.0E-03	BE250103.1	EST_HUMAN	605942604.F1 NH1_MGC_13 Homo sapiens cDNA clone IMAGE:2859513 5'
4231	14128		0.87	6.0E-03	N58946.1	EST_HUMAN	Y62810.x1 Soares multiple sclerosis, 2NBHMSF Homo sapiens cDNA clone IMAGE:278178 3'
4367	14495	24271	1.37	6.0E-03	A101883.1	EST_HUMAN	Y62810.x1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1639724 3'
4597	14693	24758	0.82	6.0E-03	A1324342.1	EST_HUMAN	EST27110 Corallium l Homo sapiens cDNA 5' and similar to EST containing Alu repeat
8119	14693	24758	1.89	6.0E-03	AL163291.2	NT	Homo sapiens chromosome 21 segment HS21C081
8129	14698	24757	0.89	6.0E-03	A1630972.1	EST_HUMAN	G95520.x1 Soares parathyroid tumor, NBHFA Homo sapiens cDNA clone IMAGE:1404358 3'
8500	16358	25542	1.87	6.0E-03	AF128594.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exon 7-16 and complete cds
6586	16498	26657	7.04	6.0E-03	A103980.1	EST_HUMAN	contains MER10.01 MER10 repetitive element;
6650	16530	26724	2.44	6.0E-03	A17796337.1	EST_HUMAN	RC3-UM0057-121030-032-902 UM0057 Homo sapiens cDNA
6689	16566		1.41	6.0E-03	BF1036108.1	EST_HUMAN	601464915.F1 NH1_MGC_36 Homo sapiens cDNA clone IMAGE:3886028 5'
7609	17207	27506	8.21	6.0E-03	D10543.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
7776	17628		1.94	6.0E-03	A432661.1	EST_HUMAN	h2202.x1 NCI CGAP 1Kd11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
7949	17796	28039	1.5	6.0E-03	X63396.1	NT	P40429.038 REDOVAL PROTEIN L13A ;
7748	17796	28039	1.5	6.0E-03	X63396.1	NT	M thermophilum complete plasmid pPV1 DNA
8127	18015	28263	2.23	6.0E-03	A15932164.1	EST_HUMAN	EST374237 MAGC neoplasia, MAGC Homo sapiens cDNA
8186	18072		2.21	6.0E-03	11649814	NT	Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA
8220	18102	28346	1.89	6.0E-03	A430786.1	EST_HUMAN	h61c12.x1 NCI CGAP F128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR-O00519 O00519
8220	18102	28347	1.89	6.0E-03	A430786.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
8350	18227		3.91	6.0E-03	U14560.1	NT	h61c12.x1 NCI CGAP F128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR-O00519 O00519
8351	18228	28479	3.54	6.0E-03	BE37895.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
							Mus musculus zinc-finger protein mRNA, complete cds
							601574246.F1 NH1_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9185	18922		1.59	6.0E-03	AF010486.1	NT	Phocodacter capellatus strain SB1003, partial genome
9310	19519		3.6	6.0E-03	AF000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 460290 (section 39 of 148) of the complete genome
9372	19038		1.34	6.0E-03	AB029395.1	NT	Anguilla japonica mRNA for actin B, complete cds
9392	19583		2.21	6.0E-03	U00760.1	NT	Pneumococcus carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pcr1) gene, complete cds
9722	19222		1.57	6.0E-03	BE768019.1	EST_HUMAN	801482621F1 NH1.MGC.58 Homo sapiens cDNA clone IMAGE385588 5'
9741	19274		1.34	6.0E-03	AJ245480.1	NT	Erastria napus sgl gene for S-locus glycoprotein, cultivar T2
653	10599	20406	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF6; aminocyclo-RNA synthase, complete cds; complete ORF6, and gpeE-like protein, complete cds
653	10599	20407	1.9	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF6; aminocyclo-RNA synthase, complete cds; complete ORF6, and gpeE-like protein, complete cds
654	10599	20408	2.92	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF6; aminocyclo-RNA synthase, complete cds; complete ORF6, and gpeE-like protein, complete cds
654	10599	20407	2.92	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF6; aminocyclo-RNA synthase, complete cds; complete ORF6, and gpeE-like protein, complete cds
1008	11012	20854	1.38	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase RH3
1652	11487		0.91	5.0E-03	AJ038977.1	EST_HUMAN	g794056.x1 Soares, leads, NHT Homo sapiens cDNA clone IMAGE1735680 3'
2848	12515	23405	3.44	5.0E-03	AB033008.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2908	12532	23029	0.85	5.0E-03	BE283087.1	EST_HUMAN	801151785F1 NH1.MGC.7 Homo sapiens cDNA clone IMAGE2339199 5'
3077	13024	22820	4.08	5.0E-03	T67623.1	NT	9011809.x1 Soares Infant brain N1B Homo sapiens cDNA clone IMAGE22386 3'
3116	13041		1.75	5.0E-03	AL161491.2	NT	Atadp3a thaliana DMT chromosome 4, coding fragment No. 3
3129	13054	22883	1.04	5.0E-03	R17194.1	EST_HUMAN	g79502.x1 Soares breast 28N184 Homo sapiens cDNA clone IMAGE156568 3'
3240	13163		1.08	5.0E-03	AJ297857.1	NT	Homo sapiens partial LINC71 gene for LIM domain containing protein 1B (ponB) gene, complete cds
3041	13505	23341	4.16	5.0E-03	U08914.1	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3986	13612	23395	0.83	5.0E-03	AJ147449.2	NT	Citrus aurantiensis seed storage protein cDNA 9' end
3890	13601		1.38	5.0E-03	AJ239975.1	EST_HUMAN	EST112218 Uterus tumor 1 Homo sapiens cDNA 9' end
4207	14106	23848	0.93	5.0E-03	AJ039567.1	EST_HUMAN	Y97910.1 Soares fetal liver spleen NF1LS Homo sapiens cDNA clone IMAGE240095 5'
4209	13612	23396	0.91	5.0E-03	U08914.1	NT	Citrus aurantiensis seed storage protein cDNA, complete cds
4503	14366	24181	0.94	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4619	14507	24296	2.49	5.0E-03	AF752367.1	EST_HUMAN	ent5c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone N1HTBC_c015c02 random
5541	15458	25528	5.34	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

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Probe SEQ ID NO:	Ena SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5885	16564	25685	2.43	5.0E-03	000307	SWISSPROT	UBIQUITIN CARBOXY-TERMINAL HYDROLASE FA-FY (UBIQUITIN THIOLESTERASE FA-FY) (UBIQUITIN-SPECIFIC PROCESSING PROTEINASE FA-FY) (UBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEINASE 9, Y CHROMOSOME)
5897	16891		6.17	5.0E-03	BE520009.1	EST_HUMAN	60094469471 NIH MGC: 17 Homo sapiens cDNA clone IMAGE:2980871 3'
5971	15101	24877	6.02	5.0E-03	AB023024.1	NT	Homo sapiens MAS1 mRNA, complete cds
6566	16424	29005	6.38	5.0E-03	AB071681.6	NT	Homo sapiens MAS1 mRNA, complete cds
8794	16773	29835	1.97	5.0E-03	A480382	SWISSPROT	BEFA-GALACTOSIDASE PRECURSOR (LACTASE)
7005	16883		6.92	5.0E-03	M01132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8103	17263		7.44	5.0E-03	T10988.1	EST_HUMAN	304F Heart Homo sapiens cDNA clone 684
8310	18187	28435	3.17	5.0E-03	AW170334.1	EST_HUMAN	kn05645.x1 Soares, NIH/CC, cervical tumor Homo sapiens cDNA clone IMAGE:2980430 3' similar to contains L1 L2 L1 repetitive element
8310	18187	28438	3.17	5.0E-03	AW170334.1	EST_HUMAN	kn05645.x1 Soares, NIH/CC, cervical tumor Homo sapiens cDNA clone IMAGE:2980430 3' similar to contains L1 L2 L1 repetitive element
8399	18275	29527	1.05	5.0E-03	U41953.1	EST_HUMAN	U00804.11 Striatum placenta (857/225) Homo sapiens cDNA clone IMAGE:708850 5'
8433	18307	29563	1.73	5.0E-03	U084793	NT	U00804.11 Striatum placenta (857/225) Homo sapiens cDNA clone IMAGE:708850 5'
8644	18508		3.73	5.0E-03	BE048085.1	EST_HUMAN	MS muscle hypodermal protein, MN-C3-4760 (LOC3212), mRNA
9327	19708		5.04	5.0E-03	AF07874.1	NT	t2460-04 Y1 NC1 OGAF Brn52 Homo sapiens cDNA clone IMAGE:2281822 5'
9460	19391		8.95	5.0E-03	AF067283.1	NT	Galactin glycosylated-3-phosphate dihydrogenase mRNA, complete cds
9555	19153		1.55	5.0E-03	L10347.1	NT	Bugain gallus 1 chromosome marker
9692	19174		1.29	5.0E-03	AA485987.1	EST_HUMAN	Human pro-alpha type II collagen (COL2A1) gene, exons 1-54, complete cds
9619	18529		4.18	5.0E-03	BF572332.1	EST_HUMAN	SW-DNA2, MOUSE P14938 PROBABLE DIPHENOXOL OXIDASE, AS A COMPONENT 1
9791	19301	25197	1.94	5.0E-03	AA149105.1	EST_HUMAN	8020777471 NIH MGC: 62 Homo sapiens cDNA clone IMAGE:4258002 5'
9908	19801		1.4	5.0E-03	Q02338	SWISSPROT	U1H83-4445-08-0-3 3' NCL C3343, 5' end
9929	19400		1.41	5.0E-03	AA688708.1	EST_HUMAN	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
232	12021	20015	2.97	4.0E-03	AW501986.1	EST_HUMAN	h27400-05 Soares, NIH/CC, lung, NHL 19W Homo sapiens cDNA clone IMAGE:2734215 3'
318	10280	20077	2.18	4.0E-03	RA4462.1	EST_HUMAN	U1H8-590-06-0-3 5' U3-4-1771 NIH MGC: 50 Homo sapiens cDNA clone IMAGE:309688 3'
436	10390	20023	0.94	4.0E-03	PE4675	SWISSPROT	h27400-05 Soares, NIH/CC, lung, NHL 19W Homo sapiens cDNA clone IMAGE:309688 3'
588	10526	20333	3.81	4.0E-03	AA020339.1	EST_HUMAN	h27400-05 Soares, NIH/CC, lung, NHL 19W Homo sapiens cDNA clone IMAGE:309688 3'
850	10785	20437	1.81	4.0E-03	RA4462.1	EST_HUMAN	h27400-05 Soares, NIH/CC, lung, NHL 19W Homo sapiens cDNA clone IMAGE:309688 3'
863	10819		3.43	4.0E-03	AA74921.1	EST_HUMAN	h27400-05 Soares, NIH/CC, lung, NHL 19W Homo sapiens cDNA clone IMAGE:309688 3'
1133	11047	20860	32.55	4.0E-03	AA068777.1	EST_HUMAN	h27400-05 Soares, NIH/CC, lung, NHL 19W Homo sapiens cDNA clone IMAGE:309688 3'
1155	11055	20910	1.38	4.0E-03	AA794740.1	EST_HUMAN	h27400-05 Soares, NIH/CC, lung, NHL 19W Homo sapiens cDNA clone IMAGE:309688 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1281	11186	21040	1.33	4.0E-03	AI284374.1	EST_HUMAN	z8560.t11 NOL CGAP_G081 Homo sapiens cDNA clone IMAGE:707335
1508	11472		1.31	4.0E-03	AV708056.1	EST_HUMAN	AV708056 ADC Homo sapiens cDNA clone IMAGE:707335
1709	11610	21480	2.2	4.0E-03	U33472.1	NT	RefSeq noncoding type 1 astrocyte and oligodendrocyte associated protein AT1-46 mRNA, complete cds
1971	11894	21767	20.87	4.0E-03	AA020777.1	EST_HUMAN	2511803.t1 Striatum cDNA (6037204) Homo sapiens cDNA clone IMAGE:510068 5'
2220	12087		1.66	4.0E-03	BE410550.1	EST_HUMAN	BC1304161.F1 NIT MGCC 31 Homo sapiens cDNA clone IMAGE:3638510 5'
2232	12117	22019	1.46	4.0E-03	AW794746.1	EST_HUMAN	RC6-UM0014-170400-023-051 UM0014 Homo sapiens cDNA
2526	12400	22230	1.89	4.0E-03	U82111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), fibronectin protein L18a (RPI18a), Cdc42/Cdc42-dependent protein kinase (CAKIK), creatine transporter (CTTR), CDM protein (CDM), adrenoleukodystrophy protein >
2528	12400	22281	1.89	4.0E-03	U82111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), fibronectin protein L18a (RPI18a), Cdc42/Cdc42-dependent protein kinase (CAKIK), creatine transporter (CTTR), CDM protein (CDM), adrenoleukodystrophy protein >
2659	12638	22414	2.86	4.0E-03	AJ277385.1	NT	CDM protein (CDM), adrenoleukodystrophy protein >
2659	12638	22415	2.86	4.0E-03	AJ277385.1	NT	Homo sapiens polyamine-containing C14ORF4 gene
2854	12630	22418	1.02	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21084
3487	13403	23207	0.94	4.0E-03	AI185428.1	EST_HUMAN	36804.t1 NCL CGAP_C018 Homo sapiens cDNA clone IMAGE:2685276 3'
3487	13403	23208	0.94	4.0E-03	AI185428.1	EST_HUMAN	36804.t1 NCL CGAP_C018 Homo sapiens cDNA clone IMAGE:2685276 3'
3572	13468	23278	0.8	4.0E-03	Q13808	SWISSPROT	OLFACTORY RECEPTOR 6T1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3836	13468	23278	0.83	4.0E-03	Q13808	SWISSPROT	OLFACTORY RECEPTOR 6T1 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3852	13763	23566	0.85	4.0E-03	AF008888.1	NT	Mus musculus tumor susceptibility protein 101 (tag 101) gene, complete cds
3914	13823		1.79	4.0E-03	AJ01712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (end joined CDS)
4509	14402	24180	1.13	4.0E-03	AJ732754.1	EST_HUMAN	318006.J5 Striatum lung (6937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
5164	15030	24798	13.17	4.0E-03	AJ021897.1	NT	FoxP1 and mouth disease virus serotype A-12 118a capsid protein VP3
5225	15149	24816	1.89	4.0E-03	AJ005859.1	NT	Drosophila melanogaster armo27 (aroz207) mRNA, complete cds
9315	15236	25036	18.93	4.0E-03	AF16625.1	NT	Fallutin noncoding beta catenin binding protein mRNA, complete cds
9540	15457	25227	4.23	4.0E-03	P04196	SWISSPROT	Fallutin noncoding beta catenin binding protein mRNA, complete cds
9540	15457	25227	4.23	4.0E-03	P04196	SWISSPROT	Fallutin noncoding beta catenin binding protein mRNA, complete cds
9542	15459	25526	1.5	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE-RELATED TROPHOZOITE ANTIGEN PRECURSOR
9704	15672		3.23	4.0E-03	U22180.1	NT	Fallutin noncoding beta catenin binding protein mRNA, complete cds
9809	15714	25827	1.76	4.0E-03	BE548453.1	EST_HUMAN	301076015.F1 NIT MGCC 12 Homo sapiens cDNA clone IMAGE:3461854 5'
9809	15714	25827	1.76	4.0E-03	Q176405.1	NT	LY6operon esculentin like/3 protein (LTK3) mRNA, complete cds
9821	16136	26201	4.14	4.0E-03	Q02817	SWISSPROT	MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)
9960	16570	26702	3.91	4.0E-03	AJ115844.1	NT	Diphysalium discolorum A34 development protein DG1122 (DG1122) gene, partial cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit ELAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6774	10683	20841	2.02	4.0E-03	7662067	NT	Homo sapiens KIA0346 gene product (KIA0346), mRNA
7096	16333	27123	7.4	4.0E-03	AI653883.1	EST_HUMAN	hs98111.x1 Score_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains AU repetitive element
7151	17028		4.41	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7150	17036	27229	3.38	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C076
8472	18345	28509	6.84	4.0E-03	AL163200.2	NT	Homo sapiens chromosome 21 segment HS21C008
8295	19725		3.95	4.0E-03	BE61673.1	EST_HUMAN	FKM-BN0138-180500-002308 BN0138 Homo sapiens cDNA
9317	19009		2.25	4.0E-03	BE29820.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
							7474083.x1 NC1 CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3028095 5'
							element/contains element MER31 repetitive element
9528	19202		3	4.0E-03	BF224125.1	EST_HUMAN	element/contains element MER31 repetitive element
9608	19540		1.57	4.0E-03	AV191496.1	EST_HUMAN	LM22007.x1 NC1 CGAP_K4811 Homo sapiens cDNA clone IMAGE:2843932 3' similar to contains element
9670	19238		1.57	4.0E-03	AV191494.1	EST_HUMAN	LR3S repetitive element
9650	19416	25168	1.52	4.0E-03	AV191494.1	EST_HUMAN	RC3-ST0281-240400-015-03 ST0281 Homo sapiens cDNA
367	10323	20146	1.82	3.0E-03	AF11920.1	NT	Homo sapiens Glb2-associated factor 2 (GIA0571), mRNA
861	10787	20538	7.95	3.0E-03	AF11920.1	NT	Homo sapiens protein kinase G12 catalytic subunit alpha gene, exon 1
							Homo sapiens protein kinase G12 catalytic subunit alpha gene, exon 1
							h072605.x1 NC1 CGAP_P12 Homo sapiens cDNA clone IMAGE:762984 similar to contains AU repetitive element
1698	11542	21401	1.84	3.0E-03	AA48610.1	EST_HUMAN	element
2211	12597		0.87	3.0E-03	AF05306.1	NT	Homo sapiens M4G class 1 region
2248	12132		3.9	3.0E-03	Z33231.1	NT	Seneale (cv. Halo) mRNA for triphosphate isomerase
2249	12133	23229	1.12	3.0E-03	U48958.1	NT	Mus musculus insulin like growth factor gene, partial cds
2248	12133	23260	1.12	3.0E-03	U48958.1	NT	Mus musculus insulin like growth factor gene, partial cds
3983	12690		0.84	3.0E-03	Y06005.1	NT	Aradopsis thaliana prmt1 gene
3044	12571	22765	4.53	3.0E-03	U537696.1	EST_HUMAN	601237632F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3069833 5'
3112	13037	22853	2.62	3.0E-03	AV180297.1	EST_HUMAN	LC3-UM0076-240500-095-033 UM0076 Homo sapiens cDNA
3371	13290	23069	1.95	3.0E-03	U34006.1	NT	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exon 1 and 2
3379	13297		6.75	3.0E-03	Y12500.1	NT	C elegans samd6 gene
3895	13805	23591	7.43	3.0E-03	AV1762392.1	EST_HUMAN	AV1762392 MDS Homo sapiens cDNA clone MDS85501 5'
3896	13805	23592	7.43	3.0E-03	AV1762392.1	EST_HUMAN	AV1762392 MDS Homo sapiens cDNA clone MDS85501 5'
3950	13889	23532	1.98	3.0E-03	AV192278.1	EST_HUMAN	af04069 J9 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:115069 5'
4098	13960		1.34	3.0E-03	Z33231.1	NT	Seneale (cv. Halo) mRNA for triphosphate isomerase
4298	14164	23876	11.91	3.0E-03	AA11432.1	NT	Rattus norvegicus gntf gene
4417	14311	24096	4.37	3.0E-03	AS39141.1	EST_HUMAN	x08.F10.H3 conom Homo sapiens cDNA 3'
4630	14518	24309	0.88	3.0E-03	AL116067.1	EST_HUMAN	DKF2p16B0712.1_1761 (synonym: hamy2) Homo sapiens cDNA clone DKF2p16B0712 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4727	14613	24389	1.54	3.0E-03	A732754.1	EST_HUMAN	db1808.06 Statalogene lung (4637210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4745	14630	24416	7.09	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3885483 5'
5089	14659	24733	1.11	3.0E-03	4509414.1	NT	Homo sapiens RAPT, GTPase activating protein T (RAP1GAT1) mRNA
5099	14659	24734	1.11	3.0E-03	4509414.1	NT	Homo sapiens RAPT, GTPase activating protein T (RAP1GAT1) mRNA
5220	15143	24837	3.17	3.0E-03	8922469	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5410	18330	25380	1.41	3.0E-03	A124968.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5946	18951	28974	9.97	3.0E-03	AA486701.1	EST_HUMAN	set3R10.1 Scores, NHRMPu, S1 Homo sapiens cDNA clone IMAGE:813163 5'
6277	19141	29257	1.54	3.0E-03	AJ011419.1	NT	Kluyveromyces marxianus pcg23 gene for putative cytosolic permease
6442	18303	28488	3.71	3.0E-03	A3021793.1	NT	Oryza sativa gene for DZP protein, complete cds
6741	18620	28809	2.01	3.0E-03	N2580.1	EST_HUMAN	2627004.01 Scores, parathyroid, tumor, N36P1A Homo sapiens cDNA clone IMAGE:304783 3'
6828	16608	27001	1.29	3.0E-03	P31589	SWISSPROT	HEPATOGENOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2/A)
5940	18818	27011	1.57	3.0E-03	AL163368.2	NT	Homo sapiens chromosome 21 segment H521C068
6991	18608		1.38	3.0E-03	Q5C061	SWISSPROT	NONSTRUCTURAL PROTEIN V
7199	17076		8.92	3.0E-03	AW61374.1	EST_HUMAN	H9910.01 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:299131 3' similar to contains L1 L1 L1
7200	17107	27267	4.1	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85
7244	17121	27317	8.0	3.0E-03	AB16731.1	EST_HUMAN	093432.01 NCL CGAP_K03 Homo sapiens cDNA clone IMAGE:1635217 3' similar to gb-X57198_1.m1
7586	17449		3.48	3.0E-03	P08672	SWISSPROT	HISTONE H2B.2 (HUMAN)
7694	17544	27768	1.29	3.0E-03	P11369	SWISSPROT	CIRCULINOSPOROZITE PROTEIN PRECURSOR (CS)
7742	17552	27813	1.46	3.0E-03	P51589	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
7836	17686	27651	4.05	3.0E-03	AL163933.2	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8222	18104		2.69	3.0E-03	6903028	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8885	18573	28856	2.11	3.0E-03	A7006272.1	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8744	17653	28137	2.01	3.0E-03	A7060285.1	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8773	18500	28877	3.08	3.0E-03	A7044481.1	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8773	18500	28878	3.06	3.0E-03	A7044481.1	NT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
8841	18854	28942	1.93	3.0E-03	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
9088	19542		2.02	3.0E-03	AA529056.1	EST_HUMAN	promoter-5.007.7 Influenza Homo sapiens cDNA 5'
9103	18270	28780	1.54	3.0E-03	AA503154.1	EST_HUMAN	cd7B10.01 Scores, total, fetus, N32HR6, 9w Homo sapiens cDNA clone IMAGE:1622776 3' similar to contains L1, 13 MER28 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Med Stimuli (Top) HLA BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9160	16068		1.36	3.0E-03	AB00688.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
9336	16019	20260	2.33	3.0E-03	AJ206282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
904	10446	20268	0.89	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
904	10446	20268	0.89	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
788	12677		7.01	2.0E-03	T0674.1	EST_HUMAN	HL60G3T Sources fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE108341 5'
1340	11246	21104	1.93	2.0E-03	AJ20763.1	NT	Human epidermal growth factor receptor 2 (HER2) gene, exons 6 and 7
1343	11246	21100	1.99	2.0E-03	AJ20763.1	EST_HUMAN	Human epidermal growth factor receptor 2 (HER2) gene, complete cds
1333	11250	21115	12.6	2.0E-03	AF284448.1	NT	Human epidermal growth factor receptor 2 (HER2) gene, complete cds
1474	11370	21243	1.11	2.0E-03	AF48309	SWISSPROT	PLA1-ELT-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SPA-1) (CD151 ANTIGEN)
1500	11404	21283	1.91	2.0E-03	4557889	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1503	11404	21284	1.91	2.0E-03	4557889	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD) mRNA
1570	11437		4.94	2.0E-03	P29400	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
1733	11634	21502	1.38	2.0E-03	AA400138.1	EST_HUMAN	zx2410.r1 Source, total, fetal, N23F8, 9w Homo sapiens cDNA clone IMAGE789114 5'
1930	11846	21731	2.17	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2203	12030	21962	1.04	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2533	12409		4.82	2.0E-03	AY13782.1	EST_HUMAN	UHHBH-add-g-10-QJ.11 NC, CGAP, Sui3 Homo sapiens cDNA clone IMAGE277810 3'
3370	13289	23008	4.03	2.0E-03	AA400138.1	EST_HUMAN	zx2410.r1 Source, total, fetal, N23F8, 9w Homo sapiens cDNA clone IMAGE789114 5'
3378	13284	23003	1.02	2.0E-03	BF56865.1	EST_HUMAN	60219309011 NIH, MGC, 42 Homo sapiens cDNA clone IMAGE4303070 3'
3615	13539	23315	4.87	2.0E-03	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, P22, LUP2, TAP1, LUP7, TAP2, DOB, DOB2 and RIN98, 0, 13 and 14 genes
3859	13780	23572	0.92	2.0E-03	AB040602.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4024	13927	23703	2.15	2.0E-03	P03374	SWISSPROT	ENV POLYPROTEIN (CONTAINS COAT PROTEIN GP82; COAT PROTEIN GP93)
4127	14027		9.77	2.0E-03	U08491.1	NT	Rattus norvegicus 5-hydroxytryptamine receptor gene, partial cds
4448	14340	24130	1.93	2.0E-03	L42612.1	NT	Drosophila melanogaster shortwavelength class 2 (shw) mRNA, complete cds
4448	14340	24131	1.93	2.0E-03	L42612.1	NT	Drosophila melanogaster shortwavelength class 2 (shw) mRNA, complete cds
4906	14439	24285	0.94	2.0E-03	AF223901.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4912	14570		1.7	2.0E-03	AF27391.1	EST_HUMAN	por-6022.1 Source adult brain N25-4F-B55Y Homo sapiens cDNA clone IMAGE780690 3'
5017	14947		0.82	2.0E-03	AA24161.1	NT	Canis familiaris canifur gene for immunoglobulin heavy chain variable region
5194	15057	24820	1.04	2.0E-03	AY003150.1	NT	Homo sapiens intracellular glycoprotein lactin precursor, gene, complete cds
5194	15057	24821	1.04	2.0E-03	AY003150.1	NT	Homo sapiens intracellular glycoprotein lactin precursor, gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Exon Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6372	15292	26128	1.37	2.0E-03	BF21410.1	EST_HUMAN	601879366F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:410482.5'
5437	19445	26438	1.76	2.0E-03	A01493.1	NT	Homo sapiens mRNA for KIA0083 protein, partial cds
5501	15420	26442	1.87	2.0E-03	U03711.1	NT	Xenopus laevis xeflin mRNA, complete cds
5716	15624	26725	3.25	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT 'B'
5716	15624	26725	3.25	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT 'B'
5829	15735	26946	1.82	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5829	15735	26947	1.82	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-RP II) (CA-XI)
5831	15737	26949	7.14	2.0E-03	BF308187.1	EST_HUMAN	601857346F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:412148.5'
5830	15796	26374	2.2	2.0E-03	Q9LXP4	SWISSPROT	ADAM-15 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAMTS7)
5901	15797	26946	1.95	2.0E-03	X94451.1	NT	Laculentin mRNA for hsp74-RNA synthetase (Lyk4S)
5979	15894		1.35	2.0E-03	A050389.1	EST_HUMAN	wc95909.x1 Soares. Dictyostelium discoideum. NHCO Homo sapiens cDNA clone IMAGE:252217.3' similar to SW:FLR29 HUMAN P47914.6S RIBOSOMAL PROTEIN L29 contains element MSR1 negative element.
6212	15934	26129	2.88	2.0E-03	BE007685.1	EST_HUMAN	CM4-BT0309-061238-024-0611 BT0309 Homo sapiens cDNA
6901	16671	26793	2.11	2.0E-03	AW02004.1	EST_HUMAN	HF7303.x1 Soares. NF1_L1_OBG_S1 Homo sapiens cDNA clone IMAGE:2254035.3' similar to TR-Q06978 Q06978. JERKY.
6784	16693	26853	5.19	2.0E-03	N02087.1	EST_HUMAN	X94398.x1 Soares. malinocyte 2/NH4M Homo sapiens cDNA clone IMAGE:264442.3' similar to contains L1 L2 L1 repetitive element.
6784	16693	26854	5.19	2.0E-03	N02087.1	EST_HUMAN	X94398.x1 Soares. malinocyte 2/NH4M Homo sapiens cDNA clone IMAGE:264442.3' similar to contains L1 L2 L1 repetitive element.
7513	17301	27508	3.12	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMSM) (JI) (MOTENDINUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 19C-25) (TENASCIN-C) (TN-C)
7775	18256		5.41	2.0E-03	A0251376.1	EST_HUMAN	25T040081.01 NC CGAP CGBT Homo sapiens cDNA clone IMAGE:594764.3'
8379	18266		2.78	2.0E-03	M06524.1	NT	Human dyolophin gene
8779	19350	26520	1.78	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8829	18642		1.77	2.0E-03	BF330090.1	EST_HUMAN	RC3-BT0353-010800-115-gd4 BT0353 Homo sapiens cDNA
8836	18649	26936	12.17	2.0E-03	Z11740.1	NT	H-sapiens variable number tandem repeat (VNTR) locus DNA
9032	18635		2.07	2.0E-03	A025745.1	EST_HUMAN	Y09403.x1 NC CGAP K6d1 Homo sapiens cDNA clone IMAGE:2254969.3' similar to SW:VATG_MANSE Q95052 VAGULOLAR ATP SYNTHASE SUBUNIT G ;
9095	18647	29115	2.88	2.0E-03	A1571915.2	NT	Homo sapiens SEI.L1 (SEI.L1) gene, partial cds
9113	14047		4.48	2.0E-03	AJ245167.1	NT	Camelus dromedarius cytoP19 gene for immunoglobulin heavy chain variable region
9322	15703		2.78	2.0E-03	A0607665.1	EST_HUMAN	A0607666 GKC Homo sapiens cDNA clone GKC/GX005.5'

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Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BASE E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8414	15059	25276	1.59	2.0E-03	U00508.1	NT	H sapiens M1 gene for muscarinic acetylcholine receptor
9459	10387		9.92	2.0E-03	D84278.1	NT	Human DNA for CD38, exon 1
9525	15134		2.92	2.0E-03	AI189203.2	NT	Human sapiens chromosome 21 segment H527C003
9582	19599		1.57	2.0E-03	AB175937.1	EST_HUMAN	U66062.1 Soares_Med_Felle_N021F5_9w Homo sapiens cDNA clone IMAGE:2040351 3' similar to contains Alu repetitive element
9595	19247		1.27	2.0E-03	AF129756.1	NT	Homo sapiens MCH45 gene, partial cds. and CLIC1, DDAH, G6b, G6c, G8b, G8d, G8e, G8f, BAT6, G8g, CSX2b, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
9595	19521		1.65	2.0E-03	AF097960.1	EST_HUMAN	AF097960 GRC Homo sapiens cDNA clone GRC03X005 5'
432	10377	20198	1.35	1.0E-03	AF05477.1	EST_HUMAN	Y66606.1 Soares_finned_gland_N8HPG Homo sapiens cDNA clone GRC03X005 5'
812	10740	20587	2.35	1.0E-03	AF170293.1	EST_HUMAN	ie70608.1x1 Barleed codon HPLH87 Homo sapiens cDNA clone IMAGE:232334 5'
812	10740	20588	2.35	1.0E-03	AF170293.1	EST_HUMAN	ie70608.1x1 Barleed codon HPLH87 Homo sapiens cDNA clone IMAGE:232334 5'
1079	10935	20836	2.14	1.0E-03	AF065788.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENOTYL-COA HYDRATASE ;
1095	11015	20837	1.44	1.0E-03	AF054572.1	EST_HUMAN	W66940.1x1 NCI CGAP_Pant Homo sapiens cDNA clone IMAGE:252128 3'
1150	11093	20838	1.45	1.0E-03	AF052616.1	EST_HUMAN	W66940.1x1 NCI CGAP_Pant Homo sapiens cDNA clone IMAGE:252128 3'
1932	11675	21768	3.81	1.0E-03	P17808	SWISSPROT	W66940.1x1 NCI CGAP_Pant Homo sapiens cDNA clone IMAGE:252128 3'
2108	11697	21768	8.02	1.0E-03	AJ131016.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMI)
2557	12878	22879	1.15	1.0E-03	A3033117.1	NT	Homo sapiens SCL gene locus
3154	13079	22879	2.29	1.0E-03	P18915	SWISSPROT	Homo sapiens SCL gene locus
3154	13079	22880	2.26	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3262	13185	22884	1.16	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3466	13413	23218	0.79	1.0E-03	U08091.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3466	13413	23219	0.79	1.0E-03	U08091.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOGY
3814	13528		1.24	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
3855	13765	23559	1.02	1.0E-03	Z45549.1	NT	Human MUC2 gene, promoter region
4334	14231	24013	3.54	1.0E-03	BE339162.1	EST_HUMAN	Homo sapiens S/M1 gene for a single vesicle monomeric transporter, exons 14, 15
4377	14273	24054	3.77	1.0E-03	BE245556.1	EST_HUMAN	S cerevisiae chromosome X, resulting from ORF YUR149w
4564	14439	24244	0.87	1.0E-03	U29449.1	NT	TCAP12000 P-actin pre-B cell acute lymphoblastic leukemia Baylor-Hosch project-Toba Homo sapiens cDNA clone TCAP149a
							Canomacids elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	Off SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4717	14603	24388	1.78	1.0E-03	AI075485.1	EST_HUMAN	ovf504Lx1 Sources testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
4717	14603	24389	1.78	1.0E-03	AI075485.1	EST_HUMAN	ovf504Lx1 Sources testis_NHT Homo sapiens cDNA clone IMAGE:1640282 3'
4718	14604		6.23	1.0E-03	BE154057.1	EST_HUMAN	PMCH-H0339-300400-070-002 HT0339 Homo sapiens cDNA
5009	14683	24649	10.98	1.0E-03	O46409	SWISSPROT	APOLOPROTEIN A-IV PRECURSOR (APOAIV)
5103	14671	24747	2.03	1.0E-03	AV68970.1	EST_HUMAN	AV689870 GKC Homo sapiens cDNA clone GRC021E1 5'
5260	15173	24946	2.03	1.0E-03	AA200691.1	EST_HUMAN	z441471.N1 C01 CGAP CG81 Homo sapiens cDNA clone IMAGE:703548 5'
5317	16238	25042	3.05	1.0E-03	AJ009345.1	NT	Homo sapiens KV1QT1 gene
5349	16299	25096	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) US-IR2 domain encoding nuclear protein EBNA2, complete cds
5423	16299	25097	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) US-IR2 domain encoding nuclear protein EBNA2, complete cds
5423	16344	25397	1.69	1.0E-03	Q02389	SWISSPROT	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
5663	16577		4.08	1.0E-03	X07690.1	NT	Mouse nuclear gene
5759	16998		8.59	1.0E-03	11626176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIMP1), mRNA
5824	15730	25842	1.32	1.0E-03	1817791.1	EST_HUMAN	y838a11.r1 Scores fetal liver spleen TNF.LS Homo sapiens cDNA clone IMAGE:115772 5'
5867	15793		2.44	1.0E-03	AV502585.1	EST_HUMAN	OV3-NN1024-230400-171-055 NV1024 Homo sapiens cDNA
6342	16108	26259	2.44	1.0E-03	D16826.1	NT	Human gene for fourth semaphorin receptor subtype
6419	16281		1.37	1.0E-03	AJ22042.1	NT	Homo sapiens 550 kb contig between AML 1 and CBR1 on chromosome 21q22, segment 23
6503	16362	26537	1.63	1.0E-03	U52111.2	NT	Homo sapiens 928 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L16a (RPL16a), Gac-Ribitol-modulin-dependent protein kinase 9 (DUSP9), ribosomal protein L16a (RPL16a), adenovirus E1A protein 19kDa (E1A), creatine transporter (CTR1), human TRPM2 protein gene, exons 1,2 and 3
6538	16384		3.13	1.0E-03	MS3378.1	NT	Homo sapiens partial stein-1 gene
6636	16516	26707	5.35	1.0E-03	AJ247073.1	NT	Homo sapiens exosome-late protein 1 (EXL1) gene, exons 2 through 11, and complete cds
6798	16577	26867	2.39	1.0E-03	AF163980.1	NT	V-variant gene encoding vovoxopain
7175	17052		1.4	1.0E-03	Y11204.1	NT	Human class III alcohol dehydrogenase (ADH3) cDNA, complete cds
7273	17100	27345	4.27	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH3) cDNA, complete cds
7273	17100	27346	4.27	1.0E-03	M30471.1	NT	Thermotoga neopolitana alpha-4,5-galactosidase (galA) gene, complete cds
7541	17392	27602	1.85	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-4,5-galactosidase (galA) gene, complete cds
7541	17392	27603	1.85	1.0E-03	AF011400.1	NT	Thermotoga neopolitana alpha-4,5-galactosidase (galA) gene, complete cds
8098	17647	28196	22.37	1.0E-03	AW362383.1	EST_HUMAN	RC1-C10279-181059-011-459 C10279 Homo sapiens cDNA
8098	17647	28197	22.37	1.0E-03	AW362383.1	EST_HUMAN	RC1-C10279-181059-011-459 C10279 Homo sapiens cDNA
8133	18021	28238	2.44	1.0E-03	BE170590.1	EST_HUMAN	RC1-C10279-181059-011-459 C10279 Homo sapiens cDNA
8133	18021	28238	2.44	1.0E-03	BE170590.1	EST_HUMAN	RC1-C10279-181059-011-459 C10279 Homo sapiens cDNA
8198	18053		2.69	1.0E-03	AI93847.1	EST_HUMAN	UTP12.N1 NCI CGAP HS-03 Homo sapiens cDNA clone IMAGE:2246448 3' similar to TRC26795 Q28195
8497	18370		3.4	1.0E-03	AV175640.1	EST_HUMAN	AV1756409 MDS Homo sapiens cDNA clone VDS0DF11 5'
8497	18370		3.4	1.0E-03	AV175640.1	EST_HUMAN	AV1756409 MDS Homo sapiens cDNA clone VDS0DF11 5'
8646	18851	29113	2.82	1.0E-03	BE564488.1	EST_HUMAN	60143308/171 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:3918624 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9491	19108	26287	1.95	1.0E-03	9507208	NT	Rat1a noncoding transformation related protein 63 (Tip63), mRNA
9517	19887		2.15	1.0E-03	A347355.1	EST_HUMAN	IGFBP1.L1 NCL CGAP_C010 Homo sapiens cDNA clone IMAGE:2093013 3' similar to contains Au
9526	19707	24904	4.2	1.0E-03	BE76572.1	EST_HUMAN	positive element;
5131	14698	24769	0.81	9.0E-04	11910.1	NT	IGFBP1.H1 NCL CGAP_C010 Homo sapiens cDNA clone IMAGE:3972035 5'
5483	15404		1.96	9.0E-04	PR02727	SWISSPROT	Human retinoblastoma susceptibility gene exons 1-37; complete cds
7991	17412		1.43	9.0E-04	AB307263.1	NT	APOLIPROTEIN AIV PRECURSOR (APOAIV)
1472	11377		1.36	8.0E-04	AB307263.1	NT	Glycylzinc glabra gDAST mRNA for beta-amylin synthesis, complete cds
3843	13754	23548	1.27	8.0E-04	330459.1	NT	Xla1a1 mRNA for C/EBP protein
4089	13969		4.3	8.0E-04	P06347	EST_HUMAN	YF2B10.11 Sources fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:126901 5'
4359	14542	24332	2.38	8.0E-04	U28185.1	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8485	18565		2.08	8.0E-04	AA77094.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
8616	18483		2.15	8.0E-04	AB571095.1	EST_HUMAN	22424.10.s1 Sources, fetal heart, NIH/NIH9W Homo sapiens cDNA clone IMAGE:3778/4 3'
1786	11884	21582	1.91	7.0E-04	141635.1	NT	IGFBP3.L1 NCL CGAP_U02 Homo sapiens cDNA clone IMAGE:2176510 3'
2340	12330	22127	1.13	7.0E-04	U29185.1	NT	Homo sapiens CYP17 gene, 5' end
2882	12547	22437	3.28	7.0E-04	AL16310.2	NT	Homo sapiens prion protein (PrP) gene, complete cds
3243	13166	22808	1.03	7.0E-04	4885170	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
9523	15528		2.24	7.0E-04	AI176933.1	EST_HUMAN	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
8851	16893		3.2	7.0E-04	U76027.1	NT	wg3903.x1 Sources, NSF, F8, 9W, OT, PA, ST Homo sapiens cDNA clone IMAGE:2687209 3'
8871	16893	28673	2.81	7.0E-04	Z40361.1	EST_HUMAN	Homo sapiens Bruckner's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), 144-like ribosomal protein (L44), and FTP3 (FTP3) genes, complete cds
9586	19159		3.29	7.0E-04	BE077941.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA; Homo sapiens cDNA clone c-28a07 3'
9780	19300		2.72	7.0E-04	R17336.1	EST_HUMAN	CM1.B70814.11030.0-123412 B10074 Homo sapiens cDNA
9813	19321		3.28	7.0E-04	6008953	NT	WT13C0811 Sources infant brain, NIH Homo sapiens cDNA clone IMAGE:32298 5'
3877	13788	23676	1.34	6.0E-04	AB52523.1	EST_HUMAN	Homo sapiens beta2-microglobulin (beta2-microglobulin) gene, complete cds
3909	13805	23680	0.95	6.0E-04	K01315.1	NT	wt15a1.x1 NCL CGAP_K012 Homo sapiens cDNA clone IMAGE:2402876 3'
3959	13905	23981	0.95	6.0E-04	K01315.1	NT	Homo sapiens cyclin-1 pseudogene (IG-EP1) gene, 5' flanking region
4092	13962	23769	3.28	6.0E-04	U45983.1	NT	Homo sapiens cyclin-1 pseudogene (IG-EP1) gene, 5' flanking region
6590	16470		4.35	6.0E-04	F46408	NT	Homo sapiens CCR8 chemokine receptor (CCR8) gene, complete cds
7733	17593		3.13	6.0E-04	AB48507.2	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESINE (PRUCTOSE TRANSPORTER)
7800	17690	27887	2.24	6.0E-04	CG038650.1	EST_HUMAN	UC23589M2024.J1 989 (synonym: huc1) Homo sapiens cDNA clone DIF7256M2024
8776	18503	28881	2.07	6.0E-04	AL123042.1	EST_HUMAN	RC235N0120-350400-012.M11 EN0120 Homo sapiens cDNA
8952	18694	28820	6.32	6.0E-04	AV193749.1	EST_HUMAN	Homo sapiens 559 kb contig between AML1 and DBP1 on chromosome 21c22, segment 2/3
8906	18714		2.45	6.0E-04	Q01708	SWISSPROT	UH-90c-ab-09-01-01 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708928 3'
							NUCLEOSIDE PHOSPHATE KINASE B (NDK B) (NDK2-M2) (P18)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9226	19598		2.26	6.0E-04	AW390319.1	EST_HUMAN	RC3-H1280-261189-012-008 HT0289 Homo sapiens cDNA
9658	19421	25170	1.46	6.0E-04	114818157	NT	Homo sapiens cardiac channel, voltage-dependent, alpha 1 subunit (CAQNA1), mRNA
655	10572	20385	5.82	5.0E-04	O10341	SWISSPROT	HYPOPHOSPHATASE 3B 3D PROTEIN (ORF52)
1485	11360		1.83	5.0E-04	AW51844.1	EST_HUMAN	HYPOPHOSPHATASE 3B 3D PROTEIN (ORF52)
3367	13286	23085	1.42	5.0E-04	AA545831.1	EST_HUMAN	hK2r1.1 at NCBI CGAP Cor11 Homo sapiens cDNA clone IMAGE:101764 3' similar to contains A1u
5361	15281	25113	2.19	5.0E-04	AF24054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
9958	15001	28026	5.72	5.0E-04	AA150080.1	EST_HUMAN	303308.1 Stratiogene codon (5937204) Homo sapiens cDNA clone IMAGE:388683 5'
6304	19227	26387	13.6	5.0E-04	V23604.1	NT	Gorilla gorilla involucrin gene medium alpha, complete cds
6839	18519	26710	5.57	5.0E-04	AI186382.1	EST_HUMAN	qcd308.21 Soesma, pleveia, Shoshvika, 2N61-P840W Homo sapiens cDNA clone IMAGE:1728619 3'
7345	17213	27412	1.45	5.0E-04	AA49454.1	EST_HUMAN	similar to gp151602, cds1 VASQULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN) contains Alu repetitive element;
7543	17364	27800	4.68	5.0E-04	AW270598.1	EST_HUMAN	al56903.21 Soesma, testis, NH1 Homo sapiens cDNA clone IMAGE:1394357 3'
8343	18220		4.17	5.0E-04	AL048507.2	EST_HUMAN	hK2r1.1 at NCBI CGAP Cor11 Homo sapiens cDNA clone IMAGE:2768859 3'
8550	15281	25113	17.6	5.0E-04	AF24054.1	NT	DK172568M2024.11 586 (epitope tag) Homo sapiens cDNA clone DKF2Z968M2024
9184	19300		2.27	5.0E-04	AA486513.1	EST_HUMAN	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
9944	16413		1.48	5.0E-04	AA1241698.1	EST_HUMAN	xm17709.41 NCBI CGAP Cor11 Homo sapiens cDNA clone IMAGE:573875
389	10333		1.13	4.0E-04	BF241482.1	EST_HUMAN	8017693.41 NIH MGC-351 Homo sapiens cDNA clone IMAGE:2602793 3'
697	10962	20410	1.42	4.0E-04	U32748.1	NT	Hemophilus influenzae Rd strain 85 of 103 of the complete genome
829	10756	20006	1.57	4.0E-04	AI72083.1	EST_HUMAN	sc70206.11 Bacterial codon HPL187 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
829	10756	20007	1.57	4.0E-04	AI72083.1	EST_HUMAN	Q13825 ALBUKING PROTEINENOVOL COA HYDRATASE ;
1245	11354	21218	3.92	4.0E-04	AW176345.1	EST_HUMAN	sc70206.11 Bacterial codon HPL187 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR-Q13825
2037	11928	21823	1.08	4.0E-04	AL183278.2	NT	Q13825 ALBUKING PROTEINENOVOL COA HYDRATASE ;
2038	11979		1.19	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2598	12457	22348	2.73	4.0E-04	O96915	EST_HUMAN	DKF2P4440305.11 R34 (epitope tag) Homo sapiens cDNA clone DKF2Z9440305 5'
3177	13052	22850	1.85	4.0E-04	AF281074.1	SWISSPROT	SPRN-2 (SLK GUM Protein 2)
3317	13237	23041	0.84	4.0E-04	AV068624.1	EST_HUMAN	Homo sapiens nucleolin 2 (NRP2) gene, complete cds, alternatively spliced
4228	14126	23500	2.75	4.0E-04	AA4576831.1	EST_HUMAN	hK2r1.1 at NCBI CGAP Cor11 Homo sapiens cDNA clone IMAGE:961930 3' similar to gbM2121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4228	14126	23901	2.75	4.0E-04 AA578391.1	EST_HUMAN	h1010.s1 NCL CGAP_Cot Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);	
4437	14332	24121	1.28	4.0E-04 AAC36324.1	EST_HUMAN	znf508.s1 Stratiotes muscle 957209 Homo sapiens cDNA clone IMAGE:592670 3'	
5020	14893	24651	3.72	4.0E-04 BE592660.1	EST_HUMAN	60134595F1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:3578910 5'	
5132	14890	24770	0.9	4.0E-04 N45313.1	EST_HUMAN	Y78910.s1 Sources: multiple, aciclosir, 2N6HMSF Homo sapiens cDNA clone IMAGE:276643 3' similar to contains A11 repetitive element;	
6572	16549	27040	1.82	4.0E-04 N23507.1	EST_HUMAN	y36et12.s1 Sources: melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:294142 5'	
7583	17359	27655	2.79	4.0E-04 AF025599.1	EST_HUMAN	ov67m3.s1 Sources: testis, NIH Homo sapiens cDNA clone IMAGE:164434 3'	
7682	17512		1.44	4.0E-04 AF023855.1	NT	Mus musculus neuroclin-2a(17) mRNA, alternatively spliced, complete cds	
9526	19059		1.82	4.0E-04 AF24622.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced	
9677	19479		1.84	4.0E-04 Q05960	SWISSPROT	FORMIN (LIMB DEFORMITY PROTEIN)	
1391	10124	19542	3.04	3.0E-04 AL119426.1	EST_HUMAN	DKF20781J221.11781 (synonym: hanc2) Homo sapiens cDNA clone DKF20781J221.1 6'	
1391	10160	19577	2.22	3.0E-04 PA2356	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)	
862	10768	20586	1.37	3.0E-04 U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, clones 1 and 2	
1810	11077		1.16	3.0E-04 A330574.1	EST_HUMAN	h23402.s1 NCL CGAP_P72 Homo sapiens cDNA clone IMAGE:2118032 3'	
3238	13160	22386	3.37	3.0E-04 P25417	SWISSPROT	INTERCALIN B PRECURSOR	
3622	13793	23581	3.03	3.0E-04 F43416	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)	
3650	13795		1.18	3.0E-04 A271706.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2	
4711	14597		4.5	3.0E-04 BE15878.1	EST_HUMAN	PMH110338-18202-507-472 HT0339 Homo sapiens cDNA	
4764	14696	24456	0.95	3.0E-04 AY857723.1	EST_HUMAN	QY3-DT0048-22728-046-469 DT0048 Homo sapiens cDNA	
5052	14624		1.34	3.0E-04 Y11204.1	NT	V-antigen gene encoding v-oncoprotein	
5755	15643		4.82	3.0E-04 AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081	
6061	16026	26166	5.86	3.0E-04 AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078	
6869	16685	26575	3.49	3.0E-04 P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)	
7705	17655	27780	1.42	3.0E-04 AA484055.1	EST_HUMAN	zn48068.1 Sources: testis, NIH Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762	
7977	17827	28068	3.60	3.0E-04 AA781201.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);	
9118	19726	24908	2.33	3.0E-04 AA228301.1	EST_HUMAN	424956.s1 Sources: testis, NIH Homo sapiens cDNA clone 1391288 3' similar to gb:M6072 80S	
9463	19676	25068	4.32	3.0E-04 AB018922.1	NT	RIBOSOMAL PROTEIN L7A (HUMAN);	
8674	19361		2.01	3.0E-04 AL134463.1	EST_HUMAN	nc38044.1 NCL CGAP_P72 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1;L2;L1 repetitive element;	
169	10141	19567	1.18	2.0E-04 AF21796.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds	
						DKF20471.185 t1 547 (synonym: tibr1) Homo sapiens cDNA clone DKF20471.185 5'	
						Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and AOP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds	

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Single Exon Probes Expressed in Heart

Probes Seq ID NO.	Exon Seq ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description	
5028	14901	24672	1.95	1.0E-04	7620319	EST	Homo sapiens KIA0237 gene product (KIA0237), mRNA	
5029	14905	24678	0.99	1.0E-04	AI357156.1	EST_HUMAN	q12h04.41 NCI, CGAP, GC4 Homo sapiens cDNA, clone IMAGE:2003975 3'	
5030	5148	10601	0.9	1.0E-04	U72950.1	NT	3 cerebellar chromosome VII reading frame ORF YGL03b	
5031	15487	25593	1.38	1.0E-04	P09547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
5032	15487	25593	1.38	1.0E-04	P09547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
5033	16120	26283	12.71	1.0E-04	A1251080.1	EST_HUMAN	q127g10.41 NCI, CGAP, Q62 Homo sapiens cDNA, clone IMAGE:1895883 3'	
5034	62981	18128	20.283	12.47	1.0E-04	A1251080.1	EST_HUMAN	q127g10.41 NCI, CGAP, Q62 Homo sapiens cDNA, clone IMAGE:1895883 3'
5035	6484	16120	20.283	12.47	1.0E-04	A1251080.1	EST_HUMAN	q127g10.41 NCI, CGAP, Q62 Homo sapiens cDNA, clone IMAGE:1895883 3'
5036	17263	27455	2.63	1.0E-04	A180220.1	EST_HUMAN	W576983.1 Soares, NLF, T_GBC, S1 Homo sapiens cDNA, clone IMAGE:2356742 3'	
5037	7394	17263	27455	2.63	1.0E-04	Q83860	SWISSPROT	CYSTADENOT EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
5038	71253	27458	1.46	1.0E-04	Q83860	SWISSPROT	Homo sapiens phosphatidyl serine 1 (PLS CRT), mRNA	
5039	7592	17413	27628	1.78	1.0E-04	10663976	EST	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5040	7848	17698	1.78	1.0E-04	P09547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	
5041	8540	18573	2.17	1.0E-04	M26847.1	NT	Muscle alpha lactocysteine interferon gene, complete cds	
5042	8513	18721	1.98	1.0E-04	A1803268.1	EST_HUMAN	Homo sapiens mRNA for KIAA1142 protein, partial cds	
5043	9335	18824	1.84	1.0E-04	B5599769.1	EST_HUMAN	CHP-210049-130700-476-M3 C010040 Homo sapiens cDNA	
5044	9335	18824	1.84	1.0E-04	B5599769.1	EST_HUMAN	CHP-210049-130700-476-M3 C010040 Homo sapiens cDNA	
5045	9169	19165	1.65	1.0E-04	A1803226.1	EST_HUMAN	CHP-210049-130700-476-M3 C010040 Homo sapiens cDNA	
5046	953	10516	1.17	0.0E-05	A4718933.1	EST_HUMAN	q126456.11 Soares, beta1c, NHT Homo sapiens cDNA, clone 1326458 3'	
5047	13902	28678	0.8	0.0E-05	A1765206.1	EST_HUMAN	q15457.1 NCI, CGAP, Cor6 Homo sapiens cDNA, clone IMAGE:2394058 3' similar to contains MER8.1	
5048	13902	28678	0.8	0.0E-05	A1765206.1	EST_HUMAN	q15457.1 NCI, CGAP, Cor6 Homo sapiens cDNA, clone IMAGE:2394058 3' similar to contains MER8.1	
5049	15543	28632	1.47	0.0E-05	Q2607.1	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR	
5050	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5051	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5052	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5053	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5054	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5055	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5056	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5057	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5058	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5059	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5060	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5061	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5062	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5063	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5064	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5065	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5066	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5067	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5068	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5069	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5070	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5071	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5072	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5073	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5074	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5075	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5076	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5077	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5078	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5079	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5080	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5081	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5082	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5083	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5084	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5085	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5086	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5087	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5088	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5089	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5090	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5091	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5092	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5093	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5094	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5095	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5096	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5097	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5098	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5099	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5100	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5101	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5102	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5103	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5104	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5105	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5106	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5107	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5108	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5109	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5110	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5111	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5112	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5113	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5114	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5115	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5116	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5117	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5118	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5119	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5120	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5121	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5122	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5123	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5124	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5125	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5126	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5127	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5128	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5129	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5130	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5131	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5132	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5133	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5134	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5135	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5136	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5137	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5138	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5139	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5140	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5141	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5142	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5143	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5144	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5145	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5146	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5147	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5148	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5149	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5150	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5151	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5152	17294	27470	2.95	0.0E-05	D58905.1	NT	Homo sapiens gene for cdk5/p34 cyclin type-A precursor, complete cds	
5153	17294	27470						

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9011	19580		3.45	8.0E-05	AA276333.1	EST_HUMAN	z880101 st NCI_GCAP_GCB1 Homo sapiens cDNA clone IMAGE:704933 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element;
344	10303	20118	2.9	7.0E-05	AW847448.1	EST_HUMAN	RC3-CT0208-220998-011-E04 CT0208 Homo sapiens cDNA
344	10303	20119	2.9	7.0E-05	AW847448.1	EST_HUMAN	RC3-CT0208-220998-011-E04 CT0208 Homo sapiens cDNA
555	10460	20302	2.02	7.0E-05	LA8076.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HF072014
555	10460	20303	1.05	7.0E-05	LA8076.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HF072014
1035	10957	20800	2.32	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2868	12351	22440	5.24	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3121	13046	22843	5.78	7.0E-05	AB006801.1	NT	Diclytelium discoidium gene for TRFA, complete cds
4278	14175	23963	1.27	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4344	14241	24023	0.82	7.0E-05	U09080.1	NT	Ceenorhabdalis elegans Sko1p homolog mRNA, complete cds
4842	14723	24806	0.84	7.0E-05	98453001	NT	Rat cytomegaloovirus Meas1p, complete genome
5202	15065		1.12	7.0E-05	AA327812.1	EST_HUMAN	EST178713 Pilocarpine 1 Homo sapiens cDNA
7508	17268	27505	3.04	7.0E-05	T07065.1	EST_HUMAN	EST14984 Fetal brain, Striatum (cat693208) homo sapiens cDNA clone HHEB090
8501	18374		2.89	7.0E-05	10839246	NT	Homo sapiens sarcophyllin, epsilon (SGE3) mRNA
1381	18742	21769	1.37	8.0E-05	488570	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
1981	18742	21767	1.37	8.0E-05	488570	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2544	12418	22309	1.42	8.0E-05	AA56241.1	EST_HUMAN	Y6506001 NCI_GCAP_GCB1 Homo sapiens cDNA clone IMAGE:2309631 3' similar to gb.03250 DNA TOPISOMERASE (HUMAN);
2652	12519	22459	0.89	8.0E-05	224506.1	NT	H-sapiens low-sorted chromozome 8 Hscl11 fragment, SC9pA.28B10
2652	12519	22410	0.89	8.0E-05	224506.1	NT	H-sapiens low-sorted chromozome 8 Hscl11 fragment, SC9pA.28B10
2783	10568	20415	2.48	6.0E-05	AF053500.1	NT	H-sapiens low-sorted chromozome 8 Hscl11 fragment, SC9pA.28B10
5505	15519	25589	3.33	6.0E-05	Q12950	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5505	15519	25600	3.33	6.0E-05	Q12950	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
8895	15761	26709	1.49	6.0E-05	N72833.1	EST_HUMAN	Y050111.1 Scores fetal liver spleen, INF-3 Homo sapiens cDNA clone IMAGE:248212 5'
6918	16758	20669	2.81	6.0E-05	AA66629.1	EST_HUMAN	PM4-NN0060-310300-001-410 NN0050 Homo sapiens cDNA
7330	17234	27437	1.37	6.0E-05	P06807	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (CBIP)
7330	17234	27438	1.37	6.0E-05	P06807	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (CBIP)
7484	17354	27558	1.28	6.0E-05	T94146.1	EST_HUMAN	y62612121 Striatum lung (6637210) Homo sapiens cDNA clone IMAGE:119062 5'
8131	18019	28267	3.08	6.0E-05	R75936.1	EST_HUMAN	y62612121 Striatum lung (6637210) Homo sapiens cDNA clone IMAGE:119062 5'
8807	18821	28911	3.59	6.0E-05	AA044015.1	EST_HUMAN	repetitive element/contains LTR7 repetitive element;
9534	19587	25073	8.44	6.0E-05	AW980110.1	EST_HUMAN	25600208-255400-001-409 NT1038 Homo sapiens cDNA clone IMAGE:487035 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9895	19427		1.64	6.0E-05 BE688403.1	EST_HUMAN	7628408.x1 NC1_OGAP_Bm23 Homo sapiens cDNA clone IMAGE:3307768 3'	
1382	11287	21141	14.37	5.0E-05 AW352086.1	EST_HUMAN	Q14V-10234-241160-040-011 ST0234 Homo sapiens cDNA	
1819	11716		1.03	5.0E-05	6923801	NT	Homo sapiens 2302c peroxisomal membrane protein-like (LOC55895), mRNA
2831	12760	22560	0.98	5.0E-05 AJ251059.1	NT	Homo sapiens MEPTA gene, promoter region and exon 1	
3897	13293	23563	2.09	5.0E-05 AJ231894.1	NT	Homo sapiens partial SL02243 gene for extraneuronal monoamine transporter (EMT), exon 1	
5392	15311	25165	9.01	5.0E-05 X66855.1	NT	Human ML C10m1 gene for embryonic myosin alkaline light chain, 3'UTR	
5646	15559	25652	3.46	5.0E-05 AV65344.1	EST_HUMAN	AV65344 GLC Homo sapiens cDNA clone GLC04A08 3'	
6326	19173		2.96	5.0E-05 P49763	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)	
6500	19173		3.47	5.0E-05 P49763	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)	
2776	10163		4.98	4.0E-05 U12821.1	NT	Human renin (REN) gene, 5' flanking region	
7496	17366		7.17	4.0E-05 AF22635.1	NT	Homo sapiens PPT1200 mRNA, complete cds	
8150	18038	28299	4.6	4.0E-05 AW627948.1	EST_HUMAN	H9907.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2914980 3' similar to contains element MIR repetitive element;	
8287	18899		2.17	4.0E-05 AW117580.1	EST_HUMAN	x93490.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605162 3'	
695	10599	20417	0.84	3.0E-05 AJ249061.1	EST_HUMAN	q93490.x1 Soares, full_liver_spleen, INELS.S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains AU repetitive element; contains element KER repetitive element;	
1043	10801	20854	1.36	3.0E-05 BF077851.1	EST_HUMAN	x24493.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2841400 3'	
1115	11030	20870	1.28	3.0E-05 BF077868.1	EST_HUMAN	601461.635F1 NHL_MGC_06 Homo sapiens cDNA clone IMAGE:3955142 5'	
1115	11030	20871	1.28	3.0E-05 BF077898.1	EST_HUMAN	601461.635F1 NHL_MGC_06 Homo sapiens cDNA clone IMAGE:3955142 5'	
2058	12553	22442	0.91	3.0E-05 C62224	SWISSPROT	SKLEMIN	
4295	14184	23964	6.89	3.0E-05 BE169211.1	EST_HUMAN	PMH-H10521-12020-001-s10 HT0521 Homo sapiens cDNA	
4295	14184	23965	6.89	3.0E-05 BE169211.1	EST_HUMAN	PMH-H10521-12020-001-s10 HT0521 Homo sapiens cDNA	
4395	14261	24045	1.19	3.0E-05 AJ368078.1	EST_HUMAN	EST176966 Placenta 1 Homo sapiens cDNA similar to p53-associated protein	
4395	14261	24046	1.19	3.0E-05 AJ368078.1	EST_HUMAN	EST176966 Placenta 1 Homo sapiens cDNA similar to p53-associated protein	
4518	14412	24197	0.85	3.0E-05 AFI49773.1	NT	Homo sapiens NOTD1 protein (NOTD1) gene, exons 1, 2, and 3	
4731	10569	20477	0.84	3.0E-05 AJ249061.1	EST_HUMAN	q93490.x1 Soares, full_liver_spleen, INELS.S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains AU repetitive element; contains element KER repetitive element;	
5151	19018	20478	0.97	3.0E-05 AW72690.1	EST_HUMAN	AV726900 HTC Homo sapiens cDNA clone HTCC0A01 5'	
5412	15532	23582	1.54	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor (lymphocyte-specific) (Myo2b), mRNA
6011	16491	26977	2.23	3.0E-05 BE733157.1	EST_HUMAN	236905.5.1 NHL_MGC_02 Homo sapiens cDNA clone IMAGE:3942592 5'	
6803	19742	26955	1.92	3.0E-05 AA284046.1	EST_HUMAN	236905.5.1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:3942592 5'	
7134	17031	21725	1.95	3.0E-05 AW170882.1	EST_HUMAN	HT04903.x1 NC1_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009383 3'	
7138	17035	21728	1.5	3.0E-05	6912481	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
7373	17242	27447	1.33	3.0E-05 AA372692.1	EST_HUMAN	EST184475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7570	17421		3.15	3.0E-05	AI796331.1	EST_HUMAN	Wd3909.X1 Scores: NSF_F8_9W_OT_P1_X_9_S1 Homo sapiens cDNA clone IMAGE:2367206 3'
2276	12160	22056	1.76	2.0E-05	AI286021.1	EST_HUMAN	CHD4L1.1 Scores: NPL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1850552 3' similar to contains
2338	12412	22302	3.02	2.0E-05	M1702.1	NT	Human zinc finger domain (ZNF) gene, complete cds
2681	12546		7.21	2.0E-05	AA160523.1	EST_HUMAN	240401.21 Strategic INT Neuron (6037233) Homo sapiens cDNA clone IMAGE:632754 5' similar to
3096	13029	22821	1.5	2.0E-05	BE06938.1	EST_HUMAN	contains Alu repetitive element; contains element L1 repetitive element
3304	13225	23027	0.94	2.0E-05	AF184814.1	EST_HUMAN	RC3-8T0318-120200-014-008 BT0319 Homo sapiens cDNA
3323	13243	23050	1.14	2.0E-05	U62821.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3449	13368		1	2.0E-05	X62553.1	NT	H sapiens DNA for endogenous retroviral like element
3737	13946		0.85	2.0E-05	AL039107.1	EST_HUMAN	S cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
4510	14403	24191	0.69	2.0E-05	AI23349.1	EST_HUMAN	DKFZP660066.L1 155 (cynonym: Hfd2) Homo sapiens cDNA clone IMAGE:1823374 3' similar to contains
4592	14480		1.06	2.0E-05	BE379471.1	EST_HUMAN	MER18.lcd MER18 repetitive element;
4762	14556	24453	0.91	2.0E-05	AI191016.1	EST_HUMAN	601230456F NIH_JMGC_44 Homo sapiens cDNA clone IMAGE:3009553 5'
5520	15438	25023	1.42	2.0E-05	U011712.1	NT	Homo sapiens SCL gene locus
5653	15585	25022	2.19	2.0E-05	AA714330.1	EST_HUMAN	Homo sapiens TNNI1 gene, exons 1-11 (and joined CDS)
9125	15572	28108	2.19	2.0E-05	V06426.1	EST_HUMAN	mw05812.at NC1 CGAP_S31 Homo sapiens cDNA clone IMAGE:1235519 3'
9136	15593		6.04	2.0E-05	AI591026.1	EST_HUMAN	Falcatrum mRNA for AARPT protein, partial
							wc35017.X1 Scores: Dackgrafe_cotton_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
6243	15109	26200	2.21	2.0E-05	AF24382.1	NT	Heterodontus Francisel Hsd10 (HsdA10), Hsd10 (HsdA9), Hsd17 (HsdA7), HsdA6 (HsdA9), HsdA5 (HsdA5), HsdA4 (HsdA4), HsdA3 (HsdA3), HsdA2 (HsdA2), and HsdA1 (HsdA1) genes, complete cds
6243	15109	26261	2.21	2.0E-05	AF22452.1	NT	Heterodontus Francisel Hsd10 (HsdA10), HsdA9 (HsdA9), HsdA7 (HsdA7), HsdA6 (HsdA9), HsdA5 (HsdA5), HsdA4 (HsdA4), HsdA3 (HsdA3), HsdA2 (HsdA2), and HsdA1 (HsdA1) genes, complete cds
6903	15483	26971	2.3	2.0E-05	AI891040.1	EST_HUMAN	h20005.X1 NC1 CGAP_GLI1 Homo sapiens cDNA clone IMAGE:2703869 3'
8024	17674	28116	2.45	2.0E-05	N41751.1	EST_HUMAN	wk91005.l1 Scores: Idonata_Blowhole_2Nbf-FBlawV Homo sapiens cDNA clone IMAGE:250570 5'
8024	17674	28117	2.45	2.0E-05	N41751.1	EST_HUMAN	wk91005.l1 Scores: Idonata_Blowhole_2Nbf-FBlawV Homo sapiens cDNA clone IMAGE:250570 5'
8036	15983		2.42	2.0E-05	AI091025.1	EST_HUMAN	wc34907.X1 Scores: Dackgrafe_cotton_NHCD Homo sapiens cDNA clone IMAGE:252077 3'
8748	17697	28141	2.93	2.0E-05	BE176801.1	EST_HUMAN	RC5H10362-280300-012-171H10382 Homo sapiens cDNA
							mw21403.X1 NC1 CGAP_KGRT1 Homo sapiens cDNA clone IMAGE:183532 3' similar to TR:G12832
9335	19514		2.98	2.0E-05	BE346220.1	EST_HUMAN	Q12832 CLTCOPHORN HEPT2;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9442	19677		3.73	2.0E-05	AW074904.1	EST_HUMAN	x89a03.x1 NCL_OGAP_Cot1 Homo sapiens cDNA IMAGE:2673932 3' similar to contains L1 L83 L1 repetitive element;
9450	19673		2.25	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
9537	19209	28257	1.81	2.0E-05	AU131513.1	EST_HUMAN	U131513.1 NT2R23 Homo sapiens cDNA clone NT2R23002707 5'
2653	12729	22417	1.91	1.0E-05	AL163292.2	NT	Homo sapiens chromosome 21 segment HS21C082
3559	13513	23301	1.97	1.0E-05	AF068273.1	NT	Drosophila melanogaster alain Lamin 120 Suppressor of Hairless (Sul11) gene, partial cds
3859	13797	23683	9.24	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4082	13864	23761	1.09	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C033
4190	14080	23853	2.01	1.0E-05	AA431119.1	EST_HUMAN	zw56g01.1 Score, testis, NHT Homo sapiens cDNA clone IMAGE:781484 5'
4742	14627	24433	2.16	1.0E-05	AW19134.1	EST_HUMAN	yx49111.x1 NCL_OGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2695548 3'
4832	14763	24539	4.46	1.0E-05	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C049
6049	18662	23082	1.42	1.0E-05	AJ246003.1	NT	Homo sapiens Spst gene for spastin protein
6211	19993	26126	3.64	1.0E-05	AA641846.1	EST_HUMAN	nt19c23.x1 NCL_OGAP_GC81 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1 L1 L1
6213	18070	26226	6.65	1.0E-05	400844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
6572	18430		1.8	1.0E-05	P19474	SWISSPROT	53 KDa RO PROTEIN (SJOERGEN'S SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
7108	17045		2.16	1.0E-05	AL163272.2	NT	Homo sapiens chromosome 21 segment HS21C027
7240	17177	27312	2.48	1.0E-05	AA42578.1	EST_HUMAN	z50512.x1 Score, testis, NHT Homo sapiens cDNA clone IMAGE:786519 3' similar to
7382	17220	27420	11.8	1.0E-05	AA296110.1	EST_HUMAN	z50512.x1 Score, testis, NHT Homo sapiens cDNA clone IMAGE:664332 5' similar to contains A11
7704	17654	27778	1.2	1.0E-05	AW251521.1	EST_HUMAN	U1H-BE-egf-c4093-U1.g1 NCL_OGAP_S164 Homo sapiens cDNA clone IMAGE:2724398 3'
7704	17654	27779	1.2	1.0E-05	AW251521.1	EST_HUMAN	U1H-BE-egf-c4093-U1.g1 NCL_OGAP_S164 Homo sapiens cDNA clone IMAGE:2724398 3'
7651	17701		1.78	1.0E-05	AW43696.1	EST_HUMAN	1a07610.x1 NCL_OGAP_K412 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1 L2 L1
8291	18170	28414	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H-LAH) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
8291	18170	28415	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H-LAH) gene, Rofet gene, and sodium phosphate transporter (NPT3) gene, complete cds
2637	12504	22398	6.59	9.0E-06	AB53811.1	EST_HUMAN	U73a05.x1 NCL_OGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246396 3'
3057	12384	22775	3.95	9.0E-06	AJ218993.1	EST_HUMAN	qg11608.x1 Score, placenta, 800weeks, 20N6-P809W Homo sapiens cDNA clone IMAGE:1759191 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3650	13479		2.94	0.0E-06	M61765.1	NT	Human diaminohydroxyethyl aminotransferase (AGXT) gene, exons 1 and 2
5590	15613	26391	2.88	0.0E-06	U24146.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6 ox2001.x1 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:165912.3 similar to contains ARI repetitive element;
6070	16428	26011	10.24	0.0E-06	A034370.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
5931	15909	27004	1.16	0.0E-06	AF163209.2	NT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7192	17099	27257	2.81	0.0E-06	Q03769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7192	17099	27258	2.81	0.0E-06	Q03769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
7317	17193	27394	4.58	0.0E-06	Q31114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
8309	18186	28434	3.35	0.0E-06	A101064	SWISSPROT	PUTATIVE SERINE/THREONINE PROTEIN KINASE C22E12.14C
2463	12722	22251	1.65	0.0E-06	A17492396.1	EST_HUMAN	RC3-OT2263-201189-011-111 C10283 Homo sapiens cDNA
8602	18795	29087	2.24	0.0E-06	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
8602	18795	29088	2.24	0.0E-06	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
903	10886		1.7	7.0E-06	A4696729.1	EST_HUMAN	cd0010.x1 Sialoglycoprotein (SGP372.0) Homo sapiens cDNA clone IMAGE:54281.3 similar to contains MER20.11 MER20 repeat element;
1420	11320	21181	3.19	7.0E-06	A4696729.1	EST_HUMAN	Homo sapiens KIA00555 gene product (KIA00555), mRNA
2844	12722		6.86	7.0E-06	A396262.1	EST_HUMAN	4q49q40x1 NCL_GCAP_U16 Homo sapiens cDNA clone IMAGE:1991295.3 similar to contains ARI repetitive element
3516	13422		0.89	7.0E-06	A385642.1	EST_HUMAN	EST16265 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
4463	15412		5.73	7.0E-06	AY855141.1	EST_HUMAN	Q125101032250403-173401 OT10052 Homo sapiens cDNA
4072	15008	24500	5.39	7.0E-06	BT15672.1	EST_HUMAN	961816221 N1N1_MGC_37 Homo sapiens cDNA clone IMAGE:4693972.5
2897	12814	22807	1.09	0.0E-06	BE099185.1	EST_HUMAN	Q134161031910300-105-411 B10379 Homo sapiens cDNA
3655	13549	23366	1.02	0.0E-06	BE099185.1	EST_HUMAN	Q134161031910300-105-411 B10379 Homo sapiens cDNA
4647	12838	22837	1.77	0.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4933	14539	24528	2.01	0.0E-06	A140069.1	EST_HUMAN	ox08402.x1 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:1665798.3 similar to contains MER12 MER20 repetitive element;
5281	15203	24679	1.46	0.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
7670	17620		1.89	0.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-065-302 UM0070 Homo sapiens cDNA
6900	18377	25186	1.8	0.0E-06	11418197	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
5995	15904	25706	3.58	0.0E-06	AF163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5825	15731	25543	1.88	0.0E-06	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7817	17687	27907	6.9	5.0E-06	AA313620.1	EST_HUMAN	EST155456 Colon carcinoma (HOC) cell line Homo sapiens cDNA 5' end

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9795	19311	26264	4.74	5.0E-09	AI095045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library/Homo sapiens cDNA
631	10589	20380	4.41	4.0E-09	TR16267.1	EST_HUMAN	ya48033.1 Soares infant brain 11N18 Homo sapiens cDNA clone IMAGE:59254 5' similar to contains ALU repetitive element/contains L1 repetitive element ;
828	10765	20365	9.3	4.0E-09	AW103954.1	EST_HUMAN	x059412.x1 NCL CGAP_Eso2 Homo sapiens cDNA clone IMAGE:239574 3' similar to contains ALU repetitive element/contains element MER21 repetitive element ;
1312	11218	21074	5.19	4.0E-09	AI034628.1	EST_HUMAN	IB33009.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1312	11218	21075	5.19	4.0E-09	AI034628.1	EST_HUMAN	IB33009.x1 NCL CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1468	11363	21227	2.23	4.0E-09	BF395612.1	EST_HUMAN	QV21N0045-20060-250-067 NT0046/Homo sapiens cDNA
2218	12104	22008	1.22	4.0E-09	AV015407.1	EST_HUMAN	U1H-BIO-sat-705-07-UI-1 NCL CGAP_Sut1 Homo sapiens cDNA clone IMAGE:2710423 3'
3025	12063	22748	1.39	4.0E-09	AF19349.1	NT	Gallus gallus DnaK2 protein (DnaK2) mRNA, complete cds
3819	13731	23620	1.78	4.0E-09	AV144265.1	EST_HUMAN	IL3-C7021-19200-074-B03 GT0214 Homo sapiens cDNA
4702	14598	24379	1.89	4.0E-09	AI98939.1	EST_HUMAN	w84c10.x1 NCL CGAP_Bnc26 Homo sapiens cDNA clone IMAGE:242552 3' similar to contains element MER22 repetitive element ;
4800	14721	24694	1.92	4.0E-09	AL18376.2	NT	Homo sapiens chromosome 21 segment HS2:Q78
7193	16586	27177	3.11	4.0E-09	AF036950.1	NT	Homo sapiens T cell receptor beta locus, TCSEB/TS3A2 to TCSEB/V282 region
8748	17895	28139	3.74	4.0E-09	AF007951.1	NT	Homo sapiens mRNA, chromosome 1, 1p36.6, transcript K14.0436
2117	12069	21964	1.27	3.0E-09	AY06982.1	EST_HUMAN	234068.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1/L1 L1 repetitive element ;
2117	12069	21965	1.27	3.0E-09	AY06982.1	EST_HUMAN	234068.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:432863 3' similar to contains L1/L1 L1 repetitive element ;
2220	12105		1.37	3.0E-09	AF20255.1	NT	Homo sapiens PF1200 mRNA, complete cds
2991	12818	22810	0.95	3.0E-09	AI698218.1	EST_HUMAN	ai48911.x1 Soares_testis_NHT1 Homo sapiens cDNA clone IMAGE:146592 3' similar to contains LTR1.13 LTR1 repetitive element ;
3228	13152		2.14	3.0E-09	AI69779.1	EST_HUMAN	w22505.x1 NCL CGAP_UHT1 Homo sapiens cDNA clone IMAGE:2425516 3' similar to TR-060734 050734 LINE-1 LINE PROTEIN contains L1 L2 L1 repetitive element ;
3716	13529	23412	1.26	3.0E-09	BE047094.1	EST_HUMAN	hq64412.x1 NCL CGAP_HNT3 Homo sapiens cDNA clone IMAGE:3124161 3'
3716	13529	23413	1.26	3.0E-09	BE047094.1	EST_HUMAN	hq64412.x1 NCL CGAP_HNT3 Homo sapiens cDNA clone IMAGE:3124161 3'
4376	14272	24053	0.9	3.0E-09	T02063.1	EST_HUMAN	ya78010.1 Striatum ovary (8937217) Homo sapiens cDNA clone IMAGE:17275 5' similar to contains L1 repetitive element ;
4491	14355	24146	4.31	3.0E-09	X54916.1	NT	Homo sapiens gene for alpha-1-microglobulin-bikunin, locus 1.5 (encoding alpha-1-microglobulin, N-terminus)
5290	15154		1.92	3.0E-09	P08549.1	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9404	19110		4.17	3.0E-09	AV1385202.1	EST_HUMAN	RC01T0001-281199-071-A03 L70001 Homo sapiens cDNA
195	10187		3.28	2.0E-09	AF54066	SWISSPROT	HOMEOBOX PROTEIN G008002

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1550	11455		6.27	2.0E-06	F21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE] w50403.ql NCL_GGAP_K411 Homo sapiens cDNA clone IMAGE:2287088 5' similar to contains MER30.b1
2326	12207	22106	2.65	2.0E-06	A072138.1	EST_HUMAN	MER30 repeat element
2418	12255	22192	2.14	2.0E-06	FG020	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
2519	12353	22285	2.80	2.0E-06	F00719	SWISSPROT	KNOB ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3475	13351	23156	1.11	2.0E-06	A1057555.1	EST_HUMAN	A1057555 BL C Homo sapiens cDNA clone GLGEP303 3'
3700	13614	23398	1.5	2.0E-06	AAT17518.1	EST_HUMAN	AP20565.11 Singapore ovarian cancer (8637219) Homo sapiens cDNA clone IMAGE:595232 5'
3710	13623	23406	1.5	2.0E-06	A0500563.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5578	15784	25504	5.08	2.0E-06	A018424.1	EST_HUMAN	W50004.X1 NCL_GGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
7136	17013	27206	1.95	2.0E-05	H62051.1	EST_HUMAN	y40704.11 Scores over tumor N1807 Homo sapiens cDNA clone IMAGE:236974 5' similar to gb:Y74629
8403	15699	24901	1.35	2.0E-05	P23248	SWISSPROT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN)
9548	19148		2.46	2.0E-05	BE328232.1	EST_HUMAN	h52902.x1 NCL_GGAP_K413 Homo sapiens cDNA clone IMAGE:314469 3' similar to contains L12.L1 repetitive element
31	10018	18813	1.9	1.0E-05	A07682	SWISSPROT	ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH AFFINITY SODIUM-DEPENDENT CARNITINE CO-TRANSPORTER)
641	10578	20394	1.81	1.0E-05	AF054364.1	NT	Mus musculus DRAM8E protein (DRAM8) mRNA, complete cds
1435	11340	21205	2.22	1.0E-05	P09725	SWISSPROT	MEROZONTE SURFACE PROTEIN GIN28
1507	11412	21271	1.09	1.0E-05	AL183278.2	NT	Homo sapiens chromosome 21 segment HS27C078
1554	11459	21317	0.93	1.0E-05	A034141.1	EST_HUMAN	zD0612.s1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429952 3' similar to contains Alu repetitive element
1554	11459	21318	0.93	1.0E-05	A034141.1	EST_HUMAN	zD0612.s1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:429952 3' similar to contains Alu repetitive element
1595	11470		1.2	1.0E-06	P27025	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1945	11544	21729	4.74	1.0E-06	AF184014.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
1945	11544	21730	4.74	1.0E-06	AF184014.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4273	14372	20549	11.11	1.0E-06	L07651.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5043	14515	24588	1.38	1.0E-06	AL183265.2	NT	Homo sapiens chromosome 21 segment HS21C095
5043	14515	24588	1.38	1.0E-06	AL183265.2	NT	Homo sapiens chromosome 21 segment HS21C095
5253	15157	24525	4.08	1.0E-06	BF032015.1	EST_HUMAN	MR1-BT0890.030700-002-005 BT0890 Homo sapiens cDNA
6107	16001	26193	6.11	1.0E-06	F02071	SWISSPROT	FIBRINOGEN ALPHA/ALPHA CHAIN PRECURSOR
6813	16652	26851	1.16	1.0E-06	A347010.1	EST_HUMAN	q95402.x1 NCL_GGAP_Co8 Homo sapiens cDNA clone IMAGE:1026842 3'

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Single Exon Probes Expressed in Heart

Probe Seq ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6944	16822	27013	1.53	1.0E-06/AJ287878.1	EST_HUMAN	EST_HUMAN	932086.v1 NCL CGAP Lym6 Homo sapiens cDNA clone IMAGE:1982493 3' similar to contains element MIR repetitive element;
7382	17433	27477	3.72	1.0E-06/U82988.1	NT	NT	Homo sapiens shor gene, alternatively spliced products, complete cds
7582	17433	27548	3.72	1.0E-06/U82988.1	NT	NT	Homo sapiens shor gene, alternatively spliced products, complete cds
7609	17490	27676	4.86	1.0E-06/AJ132011.1	EST_HUMAN	EST_HUMAN	277068.1 Stargate clone (#937204) Homo sapiens cDNA clone IMAGE:387174 9'
7637	17688		3.73	1.0E-06/AJ46257.1	EST_HUMAN	EST_HUMAN	204471.11 Soares, NICH89.9w Homo sapiens cDNA clone IMAGE:785483 3' similar to
7588	17539		1.32	1.0E-06/AF163033.2	NT	NT	g028129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
8012	18071		4.81	1.0E-06/AF163033.2	EST_HUMAN	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C0033
8440	19077	25260	2.86	1.0E-06/U78010.1	NT	NT	RC47HT054:120501-024033 NT10054 Homo sapiens cDNA
8453	19077	25260	2.86	1.0E-06/U78010.1	NT	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
8536	19844	21729	1.84	1.0E-06/AF184714.1	NT	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
8536	19844	21730	1.84	1.0E-06/AF184714.1	NT	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
357	70314	20134	1.49	9.0E-07/AF003529.1	NT	NT	Homo sapiens glycophan 3 (GPC3) gene, partial cds and flanking repeat regions
357	70314	20135	1.49	9.0E-07/AF003529.1	NT	NT	Homo sapiens glycophan 3 (GPC3) gene, partial cds and flanking repeat regions
6572	18440	28708	2.38	9.0E-07/AF183281.2	NT	NT	Homo sapiens chromosome 21 segment HS21C0381
4661	14547	24336	4.48	8.0E-07/AJ285956.1	EST_HUMAN	EST_HUMAN	q8207.07 Soares, NHMUP.31 Homo sapiens cDNA clone IMAGE:1878876 3'
4661	14547	24337	4.48	8.0E-07/AJ285956.1	EST_HUMAN	EST_HUMAN	q8207.07 Soares, NHMUP.31 Homo sapiens cDNA clone IMAGE:1878876 3'
5580	14547	24337	7.45	8.0E-07/P21414	SWISSPROT	SWISSPROT	POLYPROTEIN CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE
6657	16547		7.89	8.0E-07/UT0770.1	NT	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
8893	18703		7.2	8.0E-07/UT0770.1	EST_HUMAN	EST_HUMAN	EST705600 Fetal brain, Stargate clone (calf093206) Homo sapiens cDNA clone HPBEN89
9055	18838		4.15	8.0E-07/AJ163260.2	NT	NT	Homo sapiens chromosome 21 segment HS21C0260
1822	17156	21566	0.94	7.0E-07/AF167341.1	NT	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (L1RAP) gene, exons 10 and 11
1870	17166	21641	2.86	6.0E-07/AF1655558.1	EST_HUMAN	EST_HUMAN	G36-CT0277.221059-024-e11 G10277 Homo sapiens cDNA
2442	12319	22217	2.41	6.0E-07/AF166493.1	NT	NT	Homo sapiens IL12 class III region containing leucine X (Tetrasich-X) gene, partial cds, cytotoxoma P450 21-
3891	13802		1.65	6.0E-07/AF141979	SWISSPROT	SWISSPROT	hydroxylase (CYP2A15), complement component C4 (C4B) G1H, helicase (SK2M), RO, complement factor B (B1) and complement component C2 (C2) genes
7279	17156	27351	1.35	6.0E-07/BF001857.1	EST_HUMAN	EST_HUMAN	HYPOHETALIC 24.1 KO PROTEIN IN LEF4-PS3 INTERGENIC REGION
8903	10284		1.81	9.0E-07/AF003222.1	EST_HUMAN	EST_HUMAN	769497.v1 NCL CGAP Cor6 Homo sapiens cDNA clone IMAGE:3374149 3' similar to TR-075620 075620
323	12023		3.55	5.0E-07/AB181893.1	EST_HUMAN	EST_HUMAN	CH4-NH1029-253000-12H-H12 NN1029 Homo sapiens cDNA
1041	10656		2.9	5.0E-07/AB030300.1	EST_HUMAN	EST_HUMAN	W64F071.1 NCL CGAP Kch11 Homo sapiens cDNA clone IMAGE:239547 3'
2095	12623		0.87	5.0E-07/AB831893.1	EST_HUMAN	EST_HUMAN	W64F071.1 NCL CGAP Kch11 Homo sapiens cDNA clone IMAGE:239547 3'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4547	14440	24223	1.44	5.0E-07	AF140774.1	NT	Homo sapiens NCO1 protein (NCO1) gene, exons 4 through 14 and complete cds
5203	15903	20096	1.71	5.0E-07	AI393981.1	EST_HUMAN	ig0805.x1 NCI CGAP CL11 Homo sapiens cDNA clone IMAGE:2107553 3' similar to contains Alu repetitive element/contains element A3R repetitive element
6203	15903	20097	1.71	5.0E-07	AI393981.1	EST_HUMAN	ig0805.x1 NCI CGAP CL11 Homo sapiens cDNA clone IMAGE:2107553 3' similar to contains Alu repetitive element/contains element A3R repetitive element
6548	16211	20373	16.83	5.0E-07	AW070885.1	EST_HUMAN	cytochrome C oxidase polypeptide (cytochrome c oxidase polypeptide) (HUMAN)
7322	17782	26021	4.11	5.0E-07	AI069887.1	EST_HUMAN	GM-BT175-220469-014 B1178 Homo sapiens cDNA
8308	18618	28003	4.31	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
8893	18673		2.05	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudocentromeric region, segment 1/2
9712	19556		2.02	5.0E-07	AW83537.1	EST_HUMAN	QYD-CT0383-210400-20-b12 C10383 Homo sapiens cDNA
9918	13627	22038	1.64	4.0E-07	AW03602.1	EST_HUMAN	w38403.x1 NCI CGAP C3 Homo sapiens cDNA clone IMAGE:2504897 3'
7335	17112	27055	5.29	4.0E-07	AW41934.1	EST_HUMAN	X49311.x1 NCI CGAP L3431 Homo sapiens cDNA clone IMAGE:2565548 3'
8308	18168	28432	3.84	4.0E-07	A176528.1	EST_HUMAN	w181083.x1 NCI CGAP K412 Homo sapiens cDNA clone IMAGE:2389703 3'
8308	18168	28433	3.84	4.0E-07	A176528.1	EST_HUMAN	w181083.x1 NCI CGAP K412 Homo sapiens cDNA clone IMAGE:2389703 3'
8552	18422		2.05	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0383-032000-030-a12 BN0383 Homo sapiens cDNA
434	10379	20200	5.01	3.0E-07	U19719.1	NT	Human ribosomal-associated glycoprotein (M1AP2) gene, putative promoter region and alternatively spliced untranscribed exons
558	10507	20314	2.38	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudocentromeric region, segment 1/2
1352	11258	21114	2.19	3.0E-07	M69146.1	NT	Human polymerase microsatellite DNA
1628	11613		2.23	3.0E-07	M84957.1	NT	Human polymerase microsatellite DNA
2000	11883		1.01	3.0E-07	AA505763.1	EST_HUMAN	ig0805.s1 NCI CGAP O12 Homo sapiens cDNA clone IMAGE:280825 similar to contains Alu repetitive element/contains L1 B1 L1 repetitive element
2342	12126	22028	1.16	3.0E-07	M89149.1	NT	Human polymerase microsatellite DNA
2420	12297	22164	17.25	3.0E-07	BE00077.1	EST_HUMAN	MPQ-BN0115-020300-001-411 BN0115 Homo sapiens cDNA
2420	12297	22165	17.25	3.0E-07	BE00077.1	EST_HUMAN	MPQ-BN0115-020300-001-411 BN0115 Homo sapiens cDNA
2998	12826	22718	0.85	3.0E-07	BE07704.1	EST_HUMAN	y60412.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA
3122	13047	22844	1.82	3.0E-07	T59704.1	SWISSPROT	HYPOPHYSAL 63.8 KD PROTEIN IN GUT1-RMT INTERGENIC REGION PRECURSOR
4624	14572	24302	7.05	3.0E-07	AW60329.1	EST_HUMAN	AV60201 GLO Homo sapiens cDNA clone GLCC0301
4554	14540	24326	0.89	3.0E-07	A197238.1	EST_HUMAN	w686412.x1 Soares NLF1 GBC S1 Homo sapiens cDNA clone IMAGE:2347907 3'
4966	14871	24634	1.47	3.0E-07	T57850.1	EST_HUMAN	yct4909.s1 Strangens lung (#63710) Homo sapiens cDNA clone IMAGE:50705 3' similar to contains Alu repetitive element/contains L1 B1 L1 repetitive element
4966	14871	24635	1.47	3.0E-07	T57850.1	EST_HUMAN	yct4909.s1 Strangens lung (#63710) Homo sapiens cDNA clone IMAGE:50705 3' similar to contains Alu repetitive element/contains L1 B1 L1 repetitive element

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6476	15366	25462	10.26	3.0E-07	088807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6028	15630	632	5.32	3.0E-07	AA81575.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6433	16294	28456	3	3.0E-07	AW167158.1	EST_HUMAN	004-010-11 NOL DGAG_GCBT Homo sapiens cDNA clone IMAGE:133680 3'
8018	18726		3	3.0E-07	AF026308.1	NT	Q17UM0036-200300-115-g2 UN0038 Homo sapiens cDNA
6559	19408		2.76	3.0E-07	AF123392.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
26	10013	19607	2.62	2.0E-07	AF263388.1	NT	Radius norvegicus mRNA for i45 kDa secretory protein, partial
148	10122	19940	4.76	2.0E-07	U77690.1	NT	Homo sapiens TRF2-interacting telomeric RAP-1 protein (RAP1) mRNA, complete cds
148	10122	19941	4.75	2.0E-07	U77690.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric and
175	10146	19982	116.1	2.0E-07	U38849.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric and
731	10983	20465	1.71	2.0E-07	AF030830.1	NT	Fugu rubripes beta-cytoplasmic (vacuolar) actin gene, complete cds
731	10983	20466	1.71	2.0E-07	AF030830.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
928	10853	20701	3.11	2.0E-07	AA222260.1	EST_HUMAN	z08807.41 Striatum NT2 neuronal precursor 987230 Homo sapiens cDNA clone IMAGE:600860 3' similar to dbL51880 ALY004H0RNA.1 PREGURSOR (HUMAN) contains Alu repetitive element
928	10854	20702	3.38	2.0E-07	T68642.1	EST_HUMAN	y15694.41 Striatum lung (987210) Homo sapiens cDNA clone IMAGE:60790 3' similar to contains L1 repeat element
1147	11060	20603	1.28	2.0E-07	Q28768	SWISSPROT	18 ADONAM18G1
1352	11485	21347	1.94	2.0E-07	Q09701	SWISSPROT	HYPOPHYSICAL 72.5 KD PROTEIN C2P7.16 IN CHROMOSOME 1
3553	13547	23334	14.74	2.0E-07	AF15348.1	NT	Homo sapiens caldesin (CADV) gene, exon 3 and partial cds
5078	14948	24723	0.87	2.0E-07	AW07066.1	EST_HUMAN	xc0807.x1 Scoree_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567485 3' similar to WP:C3842.1
5078	14948	24724	0.87	2.0E-07	AW07066.1	EST_HUMAN	CE00628 PROBABLE PARAGG DOMAINS
5198	15051	24826	0.95	2.0E-07	AL163301.2	EST_HUMAN	CE00628 PROBABLE PARAGG DOMAINS
5277	15198	24976	1.73	2.0E-07	AW98606.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C01
9009	15914	28041	1.99	2.0E-07	AF208715.1	EST_HUMAN	RC3-NM00095-200400-021-g11 NN0069 Homo sapiens cDNA
6524	16812		3.61	2.0E-07	AV726190.1	EST_HUMAN	q95605.x1 Scoree_Besla_NHT Homo sapiens cDNA clone IMAGE:1839177 3'
7627	17478		1.61	2.0E-07	AL163303.2	NT	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
7891	17741	27684	6.48	2.0E-07	AW162507.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C03
9034	19557		1.48	2.0E-07	AF72492.1	EST_HUMAN	GM4-NN0003-260300-124-c03 NN0003 Homo sapiens cDNA
1035	11022		1.21	1.0E-07	AL163262.2	NT	z085111.3d Striatum lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:550029 3' similar to contains THR_102 THR repetitive element

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar [Top Hit BLAST E Value]	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2331	12212	22110	0.94	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2403	12280	22177	0.94	1.0E-07	754818	NT	Homo sapiens RAB, member of RAS oncogene family-like 2A (RAB2A), transcript variant 2, mRNA
2797	11410	21286	1.75	1.0E-07	P06246	SWISSPROT	GLYOPROTEIN GPV
3634	11002	23874	1.33	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4195	14055	23874	2.37	1.0E-07	AV178692	EST_HUMAN	AV178692 GLC Homo sapiens cDNA clone GLCENF04 5'
4195	14055	23874	2.37	1.0E-07	AV178692.1	EST_HUMAN	AV178692 GLC Homo sapiens cDNA clone GLCENF04 5'
6103	15597	26132	5.2	1.0E-07	BEG47871.1	EST_HUMAN	IZ43405 Y1 NCL CGAP Bm32 Homo sapiens cDNA clone IMAGE:2291339 5'
6103	15597	26132	5.2	1.0E-07	BEG47871.1	EST_HUMAN	IZ43405 Y1 NCL CGAP Bm32 Homo sapiens cDNA clone IMAGE:2291339 5'
6103	15597	26132	5.2	1.0E-07	BEG47871.1	EST_HUMAN	IZ43405 Y1 NCL CGAP Bm32 Homo sapiens cDNA clone IMAGE:2291339 5'
6424	18265	28447	9.04	1.0E-07	N55081.1	EST_HUMAN	W43207.s1 Soares fetal liver spleen INFL3 Homo sapiens cDNA clone IMAGE:245484 3'
6782	18691	28850	2.91	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
6782	18691	28850	2.91	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
7180	17067	27248	3.34	1.0E-07	AA93376.1	EST_HUMAN	281010.s1 Soares fetal liver spleen INFL3 S1 Homo sapiens cDNA clone IMAGE:434340 3'
7114	17584	27700	2.37	1.0E-07	B692454.1	EST_HUMAN	6021377.14F1 NHL MGC 18 Homo sapiens cDNA clone IMAGE:427426 5'
7116	17583	27702	1.28	1.0E-07	AL386311.1	EST_HUMAN	EST186954 Brain IV Homo sapiens cDNA
7890	17830		1.98	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8364	18633	26060	3.95	1.0E-07	BEC4870.1	EST_HUMAN	IN63C11 Y1 NCL CGAP K011 Homo sapiens cDNA clone IMAGE:313212 3' similar to TRO98722 095722
8497	19173		1.37	1.0E-07	X64467.1	NT	DU116311.1
9691	18222		4.61	1.0E-07	X51755.1	NT	H1 sapiens ALAD gene for porphobilinogen synthase
7689	17659	27765	1.67	9.0E-09	AV74818.1	EST_HUMAN	Human lambda-2-immunoglobulin constant region complex (germline)
8520	18392	26656	2.81	9.0E-09	AB07082.1	EST_HUMAN	W30407.x1 NCL CGAP Gas4 Homo sapiens cDNA clone IMAGE:244932 3' similar to contains OPR12
8520	18392	26656	2.81	9.0E-09	AB07082.1	EST_HUMAN	OPR1 repetitive element
8520	18392	26656	3.91	9.0E-09	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C01
8916	19003		3.09	9.0E-09	AJ251973.1	NT	Homo sapiens fetal liver spleen
591	12671		2.95	8.0E-09	AB11382.1	EST_HUMAN	W018005.x1 Soares INFL_T GBC S1 Homo sapiens cDNA clone IMAGE:282873 3'
1034	10962		0.48	8.0E-09	BE795462.1	EST_HUMAN	601680133F1 NHL MGC 7 Homo sapiens cDNA clone IMAGE:3943976 5'
3408	13415		1.43	8.0E-09	BE795462.1	EST_HUMAN	601680133F1 NHL MGC 7 Homo sapiens cDNA clone IMAGE:3943976 5'
7074	16961	27144	3.38	9.0E-09	AF752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
7074	16961	27145	3.38	8.0E-09	AF752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
7551	17402	27616	2.99	8.0E-09	AW570933.1	EST_HUMAN	EST138276 MAGE MAGE resequences, MAGE Homo sapiens cDNA
8570	18433		2.39	8.0E-09	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
73	10057	19674	3.27	7.0E-08	002357	SWISSPROT	ANKRYR1 (ERYTHROCYTE ANKYRIN)
1338	11244	21102	12.71	7.0E-08	004806.1	NT	Rat mRNA for ribosomal protein L31
3328	13444	23240	1.09	7.0E-08	015906	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3528	13444	23241	1.09	7.0E-08	015906	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8169	18075		4.93	7.0E-08	A1635743.1	EST_HUMAN	cong3.P16 contom Homo sapiens cDNA 3'
8526	18734	25027	5.6	7.0E-08	U24076.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
9770	13444	23240	4.54	7.0E-08	015906	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9770	13444	23241	4.54	7.0E-08	015906	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
9834	19334		1.89	7.0E-08	A1131016.1	NT	Homo sapiens SCL gene locus
800	10720	20560	2.84	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
800	10720	20570	2.84	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
2312	12193	22932	1.73	6.0E-08	B144398.1	EST_HUMAN	MRO-HT0166-191169-004-g03 HT0166 Homo sapiens cDNA
4165	14055	23320	0.99	6.0E-08	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8717	18534	28518	2.26	6.0E-08	U11969	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8810	18523		1.74	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
791	10083	19380	3.95	6.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2189	12078	21581	1.97	5.0E-08	A449385.1	EST_HUMAN	ADENYDE OXIDASE
5178	15423	24500	1.12	5.0E-08	U06278	SWISSPROT	COMPLEMENT C2 PRECURSOR (C2C CONVERTASE)
6057	18599	26581	4.36	5.0E-08	U10681	SWISSPROT	Q00-CT0225-131059-004-412 CT0228 Homo sapiens cDNA
6246	18599	26317	1.94	5.0E-08	A1051678.1	EST_HUMAN	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1724	11625	21463	1.1	4.0E-08	U75723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1724	11625	21464	1.1	4.0E-08	U75723	SWISSPROT	Cricetus griseus ribosomal transcription factor (UBF) mRNA, complete cds
7279	17155	27350	1.41	4.0E-08	U42971.1	NT	ar22d10.x1 Gaster Wino tumor Homo sapiens cDNA clone IMAGE:169411 3' similar to contains Alu repetitive element/contains element MER22 repetitive element ;
7638	17788	28030	4.17	4.0E-08	A103027.1	EST_HUMAN	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNAM8 gene)
8274	18154		1.79	4.0E-08	A123847.1	NT	602248024-F1 NIH_MGC_02 Homo sapiens cDNA clone IMAGE:433300 5'
8439	18313	28570	3.86	4.0E-08	U7592483.1	EST_HUMAN	602248024-F1 NIH_MGC_02 Homo sapiens cDNA clone IMAGE:433300 5'
8439	18313	28571	3.86	4.0E-08	U7592483.1	EST_HUMAN	zdr55g3.1 Soares, Jdai, Jnoar, NHHH19W Homo sapiens cDNA clone IMAGE:346569 5' similar to contains L1.1 L1 repetitive element ;
9061	19390		1.54	4.0E-08	U79159	EST_HUMAN	IB65611.x1 NCI_G0AP_C016 Homo sapiens cDNA clone IMAGE:2652076 3' similar to contains MER18.L3
9703	19252		1.46	4.0E-08	A134333.1	EST_HUMAN	MER18 MER18 repetitive element ;

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NC	Exon SEQ ID NC	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5184	15046	24812	7.24	3.0E-08	AA191195.1	EST_HUMAN	244505.1 Striatagene INT neuron (837233) Homo sapiens cDNA clone IMAGE:502849.5
5184	15049	24813	7.24	3.0E-08	AA191195.1	EST_HUMAN	244505.1 Striatagene INT neuron (837233) Homo sapiens cDNA clone IMAGE:502849.5
5446	15367	25423	1.99	3.0E-08	BE016348.1	EST_HUMAN	5b7a10.1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:304657.0 similar to TRQ82188 Q02188 SYNTAXIN 17.
6163	15120	24904	3.58	3.0E-08	AI72937.1	EST_HUMAN	q91871.1 NCI CGAP_F28 Homo sapiens cDNA clone IMAGE:194046.5
6451	15312	26478	1.41	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS210246
6558	16416		2.97	3.0E-08	AI493482.1	EST_HUMAN	1463009.x1 Soares NSF FR_9W OT_PA_P1 S1 Homo sapiens cDNA clone IMAGE:2120273.3 similar to TRQ13837 Q13837 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ; repetitive element
9027	13519		11.6	3.0E-08	R18420.1	EST_HUMAN	Yp0204.1 Soares infant brain 11N8 Homo sapiens cDNA clone IMAGE:30848.5 similar to contains Alu
109	10171		15.76	2.0E-08	AW302996.1	EST_HUMAN	xs67008.x1 NCI CGAP_L128 Homo sapiens cDNA clone IMAGE:2767135.3
223	10184		7.67	2.0E-08	AA425598.1	EST_HUMAN	244807.1 Soares bcd_fovs_N324FR_93 Homo sapiens cDNA clone IMAGE:773317.5 similar to contains Alu repetitive element; complete cds
489	10331	20246	1.48	2.0E-08	AF19349.1	NT	Gallus gallus Dack2 protein (Dack2) mRNA, complete cds
644	10331	20268	10.93	2.0E-08	AW186438.1	EST_HUMAN	MRO-OT0060-242020-901-908 OT0060 Homo sapiens cDNA
644	10331	20297	10.93	2.0E-08	AW186438.1	EST_HUMAN	MRO-OT0060-242020-901-908 OT0060 Homo sapiens cDNA
874	10595		37.42	2.0E-08	BE280477.1	EST_HUMAN	60115532.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138592.5
1319	11226	21082	1.83	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS210247
1707	11008		1.03	2.0E-08	BE724871.1	EST_HUMAN	60157063.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199.5
1811	11708		3.99	2.0E-08	AW70271.1	EST_HUMAN	yp431.1 X1 NCI CGAP_FH11 Homo sapiens cDNA clone IMAGE:2743149.3
2388	12248	22140	1.42	2.0E-08	AA791948.1	EST_HUMAN	1463009.x1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251403.3 similar to contains L1, 18 L1 repetitive element
2495	12371		2.16	2.0E-08	K00216.1	EST_HUMAN	Shrap His-RNA-GUG
3171	13066	22601	6.02	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3171	13066	22602	6.02	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3793	13653		1.66	2.0E-08	AW1813620.1	EST_HUMAN	RC3 ST0197-161099-012-003 ST0197 Homo sapiens cDNA
3995	13953	25459	0.78	2.0E-08	U02038.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4305	14203		3.35	2.0E-08	AA48040.1	EST_HUMAN	ad06007.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:5919327.5 similar to contains L1, 12 L1 repetitive element
4876	14756		2.89	2.0E-08	AW157284.1	EST_HUMAN	ht7708.x2 NCI CGAP_CML1 Homo sapiens cDNA clone IMAGE:2919327.5 similar to contains L1, 12 L1 repetitive element
0722	18032	267931	1.31	2.0E-08	AA400721.1	EST_HUMAN	ad02008.x1 Striatagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:336974.3
8995	19799	20032	11.82	2.0E-08	BP-389604.1	EST_HUMAN	msa2205.x1 NCI CGAP_Kd11 Homo sapiens cDNA clone IMAGE:3207959.3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1463	12896	21257	1.13	1.0E-09 P31922	SWISSPROT	POL	POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONULEASE]
2035	11897		2.92	1.0E-09 BE141959.1	EST_HUMAN	PM2-HTD130-160599-001-R12	HTD130 Homo sapiens cDNA
3195	13090	22831	1.24	1.0E-09 BE246844.1	EST_HUMAN	TGAP1P52323	Podiatric pre-B cell acute lymphoblastic leukemia Baylo-HQSC project:TGBA Homo sapiens cDNA clone TCBP49522
3195	13090	22832	1.24	1.0E-09 BE246844.1	EST_HUMAN	TGAP1P52323	Podiatric pre-B cell acute lymphoblastic leukemia Baylo-HQSC project:TGBA Homo sapiens cDNA clone TCBP49522
5191	15054	24418	1.43	1.0E-09 AJ163260.2	NT	Homo sapiens chromosome 21 segment HS21C060	Homo sapiens chromosome 21 segment HS21C060
5493	15393	25414	4.05	1.0E-09 AJ010770.1	NT	Homo sapiens chromosome 21 segment HS21C060	Homo sapiens chromosome 21 segment HS21C060
6075	16582	27046	1.84	1.0E-09 AF015304.1	EST_HUMAN	HS5405.01	Scaevola jasidii_NHT Homo sapiens cDNA clone IMAGE:1618759.3
6933	16939	28773	3.66	1.0E-09 AF040983.1	EST_HUMAN	Scaevola major histocompatibility locus class III region	Homo sapiens chromosome 21 segment HS21C079
8434	18374		2.01	1.0E-09 X81755.1	NT	Human lambda-immunoglobulin constant region complex (germline)	Homo sapiens chromosome 21 segment HS21C079
8624	18515		6.3	1.0E-09 X81755.1	NT	Human lambda-immunoglobulin constant region complex (germline)	Homo sapiens chromosome 21 segment HS21C079
8884	19518		1.76	1.0E-09 BF373989.1	EST_HUMAN	NH4-S10240-240700-015-g04	S10240 Homo sapiens cDNA
4149	14049	23823	2.98	9.0E-09 AJ163279.2	NT	Homo sapiens chromosome 21 segment HS21C079	Homo sapiens chromosome 21 segment HS21C079
4149	14049	23824	2.98	9.0E-09 AJ163279.2	NT	Homo sapiens chromosome 21 segment HS21C079	Homo sapiens chromosome 21 segment HS21C079
3444	13391		1.07	8.0E-09 BE012076.1	EST_HUMAN	RQ5-BN1058-270400-031-C06	BN1058 Homo sapiens cDNA
6307	16711	26328	6.12	8.0E-09 AH185900.1	EST_HUMAN	cd2407.x1	Scores: fatal_inert_NBH119W Homo sapiens cDNA clone IMAGE:1732104.3 similar to contains MSRI.11 MSRI repetitive element;
6595	16576	26743	2.71	8.0E-09 AH185900.1	EST_HUMAN	CMD-NH1004-030300-273-g05	NH1004 Homo sapiens cDNA
7166	17073		3.06	8.0E-09 AA593892.1	EST_HUMAN	974608.31	Scores: NFL_1_GBC_S1 Homo sapiens cDNA clone IMAGE:1932576.9
3555	13409		1.08	7.0E-09 D66942.1	NT	Homo sapiens DNA for epsilon smooth muscle baine-sedn, exon 2, 3	Homo sapiens gene for epsilon smooth muscle baine-sedn, exon 2, 3
4558	14490	24236	0.99	7.0E-09 D05949.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
7355	17203	27402	3.27	7.0E-09 J60709.1	NT	G01111179ET NIH_MGC_16	Homo sapiens cDNA clone IMAGE:355183.4 5'
7350	17700	27949	1.84	7.0E-09 JE226460.1	EST_HUMAN	DNFZP45435514.T1	GAG (synonym: ItasS) Homo sapiens cDNA clone DKFZ-43C0514.5
2107	11996		1.08	9.0E-09 AL004938.1	EST_HUMAN	nfr1a1.1	NCL CGAP_HSGI Homo sapiens cDNA clone IMAGE:1046924 similar to contains L112.L1 repetitive element;
3941	13349	26255	1.06	6.0E-09 AA597940.1	EST_HUMAN	nm590B.X1	Scores: NFL_1_GBC_S1 Homo sapiens cDNA
4506	14506	24952	4.44	6.0E-09 BE169421.1	EST_HUMAN	PMH-HT0237-100200-001-H05	HT0527 Homo sapiens cDNA
4526	14526	25030	6.19	6.0E-09 AE155784.1	EST_HUMAN	nm590B.X1	Scores: NFL_1_GBC_S1 Homo sapiens cDNA
7294	17170	27370	2.26	6.0E-09	4503710 NT	Homo sapiens fibroblast growth factor receptor 3 (perlecanofasia, thanatophoric dwarfism) (FGFR3) mRNA	Homo sapiens fibroblast growth factor receptor 3 (perlecanofasia, thanatophoric dwarfism) (FGFR3) mRNA
7869	17869		4.05	6.0E-09 AF200523.2	NT	Homo sapiens basic-specific kinase substrate (TSKS) gene, complete cds	Homo sapiens basic-specific kinase substrate (TSKS) gene, complete cds
1394	11299	21157	3.09	5.0E-09 BE140284.1	EST_HUMAN	RC2-HTD252-102000-014-HTD252	Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5853	15764	25881	1.82	5.0E-06	A439464.1	EST - HUMAN	EST168746-Fetal lung H1 homo sapiens cDNA 5' end
7611	17861	27007	2.69	5.0E-09	A7769567.1	EST - HUMAN	PM21UM0053-240300-006-030 UN0053 Homo sapiens cDNA
510	10452		1.68	4.0E-09	AI163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
940	10873		2.31	4.0E-09	AI163285.2	NT	Homo sapiens chromosome 21 segment HS21C082
910	10873		0.95	4.0E-09	G959718.1	EST - HUMAN	Homo sapiens hypothetical protein (AF038169). mRNA
1483	11239	21222	0.86	4.0E-09	A4330878.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
2379	12368	22151	6.36	4.0E-09	A4330878.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
2379	12368	22151	6.36	4.0E-09	A4330878.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
2303	12184	22082	3.82	3.0E-09	BE222230.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
2906	12390	22270	1.26	3.0E-09	BE222239.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
2614	12482	22371	1.1	3.0E-09	P23249	SWISSPROT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
3287	13208	23008	3.22	3.0E-09	BE222238.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
4329	14226	24008	1.1	3.0E-09	AF17825.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
4411	14305	24068	1.54	3.0E-09	O09739.5	SWISSPROT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
7694	17754	27078	1.78	3.0E-09	AI163247.2	NT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
8384	18281	28510	3.8	3.0E-09	BE110943.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
8384	18281	28511	3.8	3.0E-09	BE110943.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
7951	10724		0.93	2.0E-09	X16574.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1227	11144	20966	6.28	2.0E-09	AI163294.2	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1637	11941		10.52	2.0E-09	AI16373.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
2278	12259		2.65	2.0E-09	O09739.5	SWISSPROT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
3859	13769	23981	3.26	2.0E-09	BE0241	SWISSPROT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
6405	16266	26128	8.9	2.0E-09	AA461430.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
7059	16832	27122	1.37	2.0E-09	AJ271735.1	NT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
8389	18457	28726	2.11	2.0E-09	AI163248.2	NT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
9676	10724		11.53	2.0E-09	X16574.1	NT	H. sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
9540	18749		1.82	2.0E-09	AA28070.1	EST - HUMAN	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
1093	11030	20350	2.48	1.0E-09	503162A	NT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
1069	11009	20351	2.48	1.0E-09	503162A	NT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
1616	11520		0.95	1.0E-09	AJ28044.1	NT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa
1616	11520		0.95	1.0E-09	AJ28044.1	NT	HS165835 Infant brain Homo sapiens cDNA 5' end and similar to similar to heat shock protein, 90 kDa

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2453	12330		0.94	1.0E-09	AB59086.1	EST_HUMAN	iq6411.x1 NO_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:204812 3' similar to contains MER12.12 MER12 repetitive element;
2880	12788	22880	1.51	1.0E-09	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (hai2) and survival motor neuron protein (smn) genes, complete cds
2895	12822	22914	3.25	1.0E-09	M28895.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2895	12822	22915	3.25	1.0E-09	M28895.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3302	12876	22974	1.23	1.0E-09	P11799	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYME (MLCK)
3302	12876	22722	0.78	1.0E-09	BE53540.1	EST_HUMAN	CONTAINS: TELONIN
4892	14678		4.28	1.0E-09	AA719297.1	EST_HUMAN	2593503.51 Sox9, phalal gland N3-HP3 Homo sapiens cDNA clone IMAGE:344577 5'
5590	15476	29549	1.37	1.0E-09	U07000.1	NT	Alu repetitive element contains element MER22 repetitive element;
6736	15944	25746	3.21	1.0E-09	P25684	SWISSPROT	Human breakpoint cluster region (BCR) gene, complete cds
7011	17781		3.11	1.0E-09	AL193893.2	NT	GRG15POROZOITE PROTEIN PRECURSOR (G5)
9478	19989	24998	2.14	1.0E-09	U1418127	NT	Homo sapiens chromosome 21 segment HS21G083
1237	11195	21048	1.8	9.0E-10	AW487740.1	EST_HUMAN	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
							MRG-S10040-059500-002-007 S10040 Homo sapiens cDNA
2853	12733	22532	6.03	9.0E-10	AI870071.1	EST_HUMAN	hw7893.41 Sox9s, Drosophila, cdna, N16C3 Homo sapiens cDNA clone IMAGE:2047285 3' similar to SW-F1023_HUMAN P27914 60S RIBOSOMAL PROTEIN L28 contains element P780 repetitive element;
6037	16032	28172	4.93	9.0E-10	AM52982.1	EST_HUMAN	U46093.21 Sox9s, Drosophila, cdna, N16C3 Homo sapiens cDNA clone IMAGE:2144637 3' similar to TR-000372 OX337 PUTATIVE P180.1;
1411	10151	19955	6.43	8.0E-10	AB59086.1	NT	Homo sapiens MORN (MORN) and DNA-PKcs (PRKDC) genes, partial cds
3300	13222	20022	2.87	1.0E-10	BE580748.1	EST_HUMAN	CV1410531-150200-071401 B10531 Homo sapiens cDNA
4106	14006	23782	0.82	8.0E-10	AA376652.1	EST_HUMAN	CV1410531-150200-071401 B10531 Homo sapiens cDNA 5' end
7725	17575		2.32	1.0E-10	U93508.2	NT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
9005	18608	28100	2.51	8.0E-10	AL193893.2	NT	Homo sapiens chromosome 21 segment HS21G083
6961	10619	20444	12.45	7.0E-10	U706225	NT	Homo sapiens TPA inducible protein (LOC15198), mRNA
6961	10619	20444	12.45	7.0E-10	U706225	NT	Homo sapiens TPA inducible protein (LOC15198), mRNA
1605	11510	21371	1.87	7.0E-10	Q13342	SWISSPROT	LYSP-100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
1374	11867		1.01	7.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2512	12369		10.88	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3049	12976	22738	2.95	7.0E-10	X00595.1	NT	H-sapiens: DHFR gene, exon 3
5754	15652	25759	3.98	7.0E-10	AA345220.1	EST_HUMAN	EF191247 Gall bladder II Homo sapiens cDNA 5' end
8514	16373		1.39	7.0E-10	P45084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
895	10821	20056	2.81	0.0E-10	AL400877.1	NT	Homo sapiens ASCL3 gene, C6BP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2644	12511	22402	1.47	0.0E-10	AL424405.1	EST_HUMAN	h62607.x1 NCL_GGAP_P128 Homo sapiens cDNA clone IMAGE:2096021 3'
4634	14522		2.81	0.0E-10	AW85718.1	EST_HUMAN	RC3-CT0254-03/1099-012.g12 CT0254 Homo sapiens cDNA
8062	18955		1.79	0.0E-10	AW971623.1	EST_HUMAN	EST1984072 MAGE sequences, MAGL Homo sapiens cDNA
9947	19397		3.54	0.0E-10	BE599410.1	EST_HUMAN	RC3-NN0070-110800-014-H07 NN0070 Homo sapiens cDNA
7441	10075		4.5	0.0E-10	AL046804.1	EST_HUMAN	DKF2p44219.1 t1431 (synonym: hlex3) Homo sapiens cDNA clone DKF2p44219.5'
3400	13347	23152	1.48	0.0E-10	001033	SWISSPROT	HYPOPHYSICAL GENE 48 PROTEIN
6334	15197		1.82	0.0E-10	BF105150.1	EST_HUMAN	601822184.F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
7465	17265	27570	1.79	0.0E-10	P34676	SWISSPROT	HYPOPHYSICAL 97.9 KD PROTEIN ZK683.9 IN CHROMOSOME III
7466	17266	27571	1.79	0.0E-10	P34676	SWISSPROT	HYPOPHYSICAL 97.9 KD PROTEIN ZK683.9 IN CHROMOSOME III
105	10087		0.99	0.0E-10	AL21083.1	EST_HUMAN	similar to contains LTR.b2 LTR repetitive element :
1951	11548	21732	1.4	0.0E-10	AW594709.1	EST_HUMAN	h65903.x1 NCL_GGAP_G08 Homo sapiens cDNA clone IMAGE:294844 3' similar to contains ALU repetitive element
2627	12401	22392	0.99	0.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6256	16125	26278	19.23	0.0E-10	AF224696.1	NT	Homo sapiens myopodictes beta A, lycosoma (MYNBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8456	18310		7.7	0.0E-10	AF003328.1	NT	Homo sapiens X-linked arylsulphatase deficiency protein gene (EDA), exon 2 and flanking repeat regions
897	10222	20086	1.72	0.0E-10	N58113.1	EST_HUMAN	Y5206.a1 Soares melanocyte 2NHJM Homo sapiens cDNA clone IMAGE:272993 3' similar to contains L1.1 L1 repetitive element :
1326	11236		5.51	0.0E-10	AY005150.1	NT	Homo sapiens extracellular glycoprotein, keratin precursor, gene, complete cds
4455	14330	24117	1.1	0.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C003
4455	14330	24118	1.1	0.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C003
5765	15072	25779	2.83	0.0E-10	P20390	SWISSPROT	RHOMBOID PROTEIN (VEINLET PROTEIN)
5933	15739	26951	3.27	0.0E-10	BE303970.1	EST_HUMAN	h67406.x1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2060319 5'
6562	16420	26559	1.31	0.0E-10	AW743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFGD008 5'
6562	16420	26560	1.31	0.0E-10	AW743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFGD008 5'
7097	16544	27136	1.58	0.0E-10	H87208.1	EST_HUMAN	y574912.a1 Soares retina V2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element :
7233	17110	27302	1.47	0.0E-10	AW650731.1	EST_HUMAN	IL3-CT0219-100200-054-B06 CT0219 Homo sapiens cDNA
7233	17110	27303	1.47	0.0E-10	AW650731.1	EST_HUMAN	IL3-CT0219-100200-054-B06 CT0219 Homo sapiens cDNA
7679	17620		2.55	0.0E-10	U69931.1	EST_HUMAN	y511612.1 Shiga toxin lung (#937210) Homo sapiens cDNA clone IMAGE:80395 5'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
281	10228	20042	1.2	9.0E-11	BE146000.1	EST_HUMAN	IL2-H10203-291069-016-c08 H10203 Homo sapiens cDNA
2057	11947	21843	6.43	9.0E-11	AL134395.1	EST_HUMAN	DKF2p47D225.11 547 (synonym: fibr1) Homo sapiens cDNA clone DKF2p47D225.5
2057	11947	21844	6.43	9.0E-11	AL134395.1	EST_HUMAN	DKF2p47D225.11 547 (synonym: fibr1) Homo sapiens cDNA clone DKF2p47D225.5
3337	13257	23064	2.25	9.0E-11	AL134395.1	EST_HUMAN	DKF2p47D225.11 547 (synonym: fibr1) Homo sapiens cDNA clone DKF2p47D225.5
3337	13257	23065	2.25	9.0E-11	AL134395.1	EST_HUMAN	DKF2p47D225.11 547 (synonym: fibr1) Homo sapiens cDNA clone DKF2p47D225.5
4400	14295	24079	1.09	9.0E-11	AA175685.1	EST_HUMAN	ae78001.s1 Stalagmus schizos brain S11 Homo sapiens cDNA
5421	15342		4	9.0E-11	BE07980.1	EST_HUMAN	RC8-B1057-140200-011-E08 B10527 Homo sapiens cDNA
8410	19062	23512	2.69	9.0E-11	C16353.1	EST_HUMAN	C16353 Clontech human acta polyA+ mRNA (46572) Homo sapiens cDNA clone IMAGE:505308 5'
3078	13005		9.97	8.0E-11	H19871.1	EST_HUMAN	Y59311.s1 Sox2s adult brain N26581855 Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element
3881	13762	23580	0.83	8.0E-11	AA178617.1	EST_HUMAN	trn5402411 NCL CGAP_Kdrl1 Homo sapiens cDNA clone IMAGE:191836 3'
3957	13865	23841	4.03	8.0E-11	N23712.1	EST_HUMAN	ww46953.s1 Weinmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255398 3'
1431	11336	21202	2.11	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 5 week Homo sapiens cDNA 5' end
6949	16827	27020	2.55	7.0E-11	AF163854.1	NT	Homo sapiens SV40 transf. (SV40) genes, complete cds, alternatively spliced
7873	17728		1.22	7.0E-11	P41389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE, ENDONUCLEASE]
8545	19145		1.31	7.0E-11	AY701686.1	EST_HUMAN	AY701686.D08 Homo sapiens cDNA clone ADBA5C09 5'
408	10352	20180	8.16	6.0E-11	M85270.1	NT	Human matrix Gla protein (MGCP) gene, complete cds
408	10352	20181	5.16	6.0E-11	M85270.1	NT	Human matrix Gla protein (MGCP) gene, complete cds
8528	16358	26568	3.88	6.0E-11	P06847	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6871	19750	26945	6.49	6.0E-11	AV727690.1	EST_HUMAN	AY727699 HTC Homo sapiens cDNA clone HTCA509 5'
11	9997	19788	0.82	6.0E-11	AL163383.2	NT	Homo sapiens chromosome 21 segment HS21C083
3320	6967	19788	1.48	6.0E-11	AL163383.2	NT	Homo sapiens chromosome 21 segment HS21C083
4195	14035	23811	1.49	6.0E-11	P48034	SWISSPROT	ALDH4YD OXIDASE
5928	15831	26954	1.69	6.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
8446	16307	28472	14.90	5.0E-11	AL260880.1	NT	Homo sapiens proboscoid beta 3 (PDBH3), mRNA
8875	18780	28072	1.79	6.0E-11	AA269042.1	EST_HUMAN	Homo sapiens KIAA0851 gene (partial), X73 gene and LZTF1 gene
1350	11285		1.4	4.0E-11	AA430042.1	EST_HUMAN	z00101211 Source: testis, NHT Homo sapiens cDNA clone IMAGE:730559 5'
2780	12822	22514	8.45	4.0E-11	BE858000.1	EST_HUMAN	0015012131 NHL_MGC_71 Homo sapiens cDNA clone IMAGE:3909285 5'
4518	14411	24166	1.37	4.0E-11	D14466.1	EST_HUMAN	HUMSPY0059 Homo brain cDNA Homo sapiens cDNA clone 069
5957	15803	25927	2.94	4.0E-11	P20095	SWISSPROT	PRE-MRN5 SPLICING FACTOR RNA HELICASE PRP2
6352	16225		3.86	4.0E-11	AF224039.1	NT	Homo sapiens marinobufalgin, beta 4, Yeoscent (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
7405	17722		1.59	4.0E-11	BE146925.1	EST_HUMAN	RC1-H10236-210100-013-008 H10256 Homo sapiens cDNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Htt BLAST E Value	Top Htt Accession No.	Top Htt Database Source	Top Htt Descriptor
9511	19190	25332	1.83	4.0E-11	11648732	NT	Homo sapiens SH3 domain binding protein 1 (SH3BP1), mRNA
1476	13479	21245	1.15	3.0E-11	6970077	NT	Mus musculus expressed in non-mesodermal cells 2, protein (NM238) (Nm23), mRNA
4179	14071		2.46	3.0E-11	AJ309248.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
							qf6604.x1 Scores, besta, JHHT Homo sapiens cDNA clone IMAGE:1782102 3' similar to contains MER10.13
944	10869	20716	1.89	2.0E-11	AJ160502.1	EST_HUMAN	YK3012.1 Scores infant brain TNIS Homo sapiens cDNA clone IMAGE:35144 5'
1168	11080	20625	3.64	2.0E-11	R24807.1	EST_HUMAN	YK3012.1 Scores infant brain TNIS Homo sapiens cDNA clone IMAGE:35144 5'
1168	11080	20627	3.64	2.0E-11	R24807.1	EST_HUMAN	Gallus gallus (fco-globin, beta-H globin, beta-A globin, epsilon-globin, and epsilon-globin-like protein
1596	11500	21359	3.91	2.0E-11	L17432.1	NT	COR3beta (COR3beta), gene, complete cds
1596	11500	21359	3.91	2.0E-11	L17432.1	NT	Gallus gallus (fco-globin, beta-H globin, beta-A globin, epsilon-globin, and epsilon-globin-like protein
1600	11505	21355	1.04	2.0E-11	AJ128371.1	EST_HUMAN	q51010.x1 Scores, pregnant uterus, NHGPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to
2176	12669	22493	1.11	2.0E-11	AF076913.1	NT	g51010.x1 Scores, pregnant uterus, NHGPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to
3160	13065	22699	4.23	2.0E-11	P10863	SWISSPROT	L1 repetitive element:
3384	13205	23005	0.97	2.0E-11	AJ478617.1	EST_HUMAN	Human endogenous retrovirus, HERV-P, 1.7D
							RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							tm54003.x1 NCJ_GGAP_K3d11 Homo sapiens cDNA clone IMAGE:2761938 3'
3452	13368		0.95	2.0E-11	AF025033.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
4501	14365		0.97	2.0E-11	AL163272.2	NT	Homo sapiens chromosome 21 segment H3210227
4551	14732		5.40	2.0E-11	BE022538.1	EST_HUMAN	Q12510255-251069-014-401 B10258 Homo sapiens cDNA
							EST178228 Odon carthageni (HOC) cell line Homo sapiens cDNA 5' end similar to similar to alpha-2-
4651	14838	24604	1.32	2.0E-11	AJ307931.1	EST_HUMAN	microglobulin
							ncs300501.1 NCJ_GGAP_GCT1 Homo sapiens cDNA clone IMAGE:797493 5' similar to SW.FR10_YEAST
8510	15715	25628	1.83	2.0E-11	AJ561028.1	EST_HUMAN	P15988 PRE-MRNA SPlicing FACTOR RNA HELICASE PRP16;
7318	17164		1.43	2.0E-11	AJF03008.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7900	17750	27699	4.61	2.0E-11	Q13306	SWISSPROT	OLFACTORY RECEPTOR 5H (OLFACTORY RECEPTOR-LIKE PROTEIN OLFI)
8457	18330	28591	2.07	2.0E-11	AJ003598.1	EST_HUMAN	2627602.x1 Scores, pregnant, uterus, NHGPU Homo sapiens cDNA clone IMAGE:471794 3'
8457	18330	28592	2.07	2.0E-11	AJ003598.1	EST_HUMAN	2627602.x1 Scores, pregnant, uterus, NHGPU Homo sapiens cDNA clone IMAGE:471794 3'
9100	19079		1.29	2.0E-11	AJ704195.1	EST_HUMAN	271703.x1 Scores, fetal liver, spleen, 1NFLS, S'; Homo sapiens cDNA clone IMAGE:100924 3'
9102	19827		2.25	2.0E-11	AJ1942143.1	EST_HUMAN	RCO-CH0027-210100-011-c01 CN0027 Homo sapiens cDNA
9216	18643	23356	1.99	2.0E-11	BF377856.1	EST_HUMAN	CM2-TN0140-070600-372-g01 TN0140 Homo sapiens cDNA
9477	19103		1.86	2.0E-11	D25217.2	NT	Homo sapiens mRNA for KIAA0027 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9627	18201		2.38	2.0E-11	P08477	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9830	19401		2.38	2.0E-11	11417969	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
9990	10584	20412	1.24	1.0E-11	AJ181018.1	NT	Homo sapiens SCL gene locus
1198	11109	20654	2.85	1.0E-11	AF163279.2	NT	Homo sapiens chromosome 21 segment HS21C076
1483	11388		1.94	1.0E-11	AF116914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2079	11969	21862	3.12	1.0E-11	AF005073.1	NT	Homo sapiens homogenitatis 1, 2-dioxygenase gene, complete cds
3454	13370	23174	1.32	1.0E-11	BE004315.1	EST_HUMAN	CHD-3N0105-17030-292-412 BN0105 Homo sapiens cDNA
5299	15191	24956	14.34	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
8773	16952	28840	3.25	1.0E-11	4885548	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
9959	16955	27090	5.41	1.0E-11	R13174.1	EST_HUMAN	Y73208.11 Sources Infant brain 1N1B Homo sapiens cDNA clone IMAGE:28168 5'
7332	17109	27300	1.32	1.0E-11	BF38518.1	EST_HUMAN	OV4-NN1149-25090-423-403 NNT149 Homo sapiens cDNA
7332	17109	27301	1.32	1.0E-11	BF38518.1	EST_HUMAN	OV4-NN1149-25090-423-403 NNT149 Homo sapiens cDNA
6507	18474	28747	1.9	1.0E-11	BF68078.1	EST_HUMAN	80215404071 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:426877 5'
9702	19483		1.28	1.0E-11	Z20377.1	EST_HUMAN	HSAAACADPH P. Human fetal Brain Whole tissue Homo sapiens cDNA
2022	12849	22649	0.92	9.0E-12	P220742	SWISSPROT	PREGNANCY ZONE PROTEIN PREGUSOR
7041	17481	27712	1.32	9.0E-12	AL153900.2	NT	Homo sapiens chromosome 21 segment HS21C100
7641	17481	27713	1.32	9.0E-12	AL153900.2	NT	Homo sapiens chromosome 21 segment HS21C100
8270	18974		3.97	9.0E-12	AJ271738.1	NT	Homo sapiens Xq pseudobacterial region, segment 2/2
4552	14454	24241	2.75	7.0E-12	Q16594	SWISSPROT	34 KD SP-DILE MATRIX PROTEIN PRECURSOR (LSM34)
8998	18548	28828	11.23	7.0E-12	AA704736.1	EST_HUMAN	325g01.s1 Sources fetal liver, spleen, TINFUS 5'-Homo sapiens cDNA clone IMAGE:461762 3'
3500	13417		0.92	8.0E-12	AV793654.1	EST_HUMAN	AT793654 HTF Homo sapiens cDNA clone HTFA7F09 5'
4252	14151	28925	7.85	8.0E-12	AA72516.1	EST_HUMAN	nz88111.s1 NCI_OGAP_G051 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element
7201	17078	27283	1.19	8.0E-12	AF003248.1	NT	Macaca fascicularis myosin heavy chain FM3A (FM3A), mRNA, complete cds
7483	17292		1.86	9.0E-12	AA847888.1	EST_HUMAN	MER29 repetitive element; 1
1027	10946	20790	2.88	5.0E-12	T06573.1	EST_HUMAN	OT10611.s1 NCI_OGAP_G081 Homo sapiens cDNA clone IMAGE:1387688 similar to contains MER29.12
3344	13204	23070	1.18	5.0E-12	BE047779.1	EST_HUMAN	tz6205.y1 NCI_OGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291217 5'
3696	13580	23367	5.03	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudobacterial region, segment 2/2
5171	15037		0.84	5.0E-12	AA720861.1	EST_HUMAN	mw24b11.s1 NCI_OGAP_G030 Homo sapiens cDNA clone IMAGE:1241973 3'
5957	15578	29576	4.75	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5957	15578	29577	4.75	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5959	16416	29540	6.12	5.0E-12	AN674760.1	EST_HUMAN	EST1368950 IMAGE rescues, MAGN Homo sapiens cDNA
7298	17145	27338	2.15	5.0E-12	AJ271735.1	NT	Homo sapiens Xq pseudobacterial region, segment 1/2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top-Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7695	17745		4.97	5.0E-12	AI163303.2	NT	Homo sapiens chromosome 21 segment HSZ1C103
244	10211	20027	3.42	4.0E-13	AA700326.1	EST_HUMAN	274q11.31 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:606978 3'
245	10211	20027	3.55	4.0E-13	AA700326.1	EST_HUMAN	274q11.31 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:606978 3'
4520	14413	24198	0.85	4.0E-12	AF03984.1	EST_HUMAN	MARNER TRANSPOSASE.1 Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
6707	16276		2.89	4.0E-12	AF16907.1	NT	Homo sapiens 690 kb contig between AML1 and CER1 on chromosome 21q22, segment 33
8451	18305	26591	3.51	4.0E-13	AF225043.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-2-galactosidase A (GLA), L44-like ribosomal protein (L44), and FTP3 (FTP3) genes, complete cds
9520	19131		1.9	4.0E-12	U76027.1	NT	1413001.X1 Soares, NFR_L_GBC_S1 Homo sapiens cDNA clone IMAGE:2609377 3' similar to TRC014617
500	10536	20345	3.81	3.0E-12	AW341983.1	EST_HUMAN	U45817 SMPR.1 1413001.X1 Soares, NFR_L_GBC_S1 Homo sapiens cDNA clone IMAGE:2609377 3' similar to TRC014617
500	10536	20345	3.81	3.0E-12	AW341983.1	EST_HUMAN	U45817 SMPR.1 1413001.X1 Soares, NFR_L_GBC_S1 Homo sapiens cDNA clone IMAGE:2609377 3' similar to TRC014617
8047	17693	28197	3.08	3.0E-12	U37072.1	NT	Human prostate specific antigen gene, 5' flanking region
8047	17693	28198	3.08	3.0E-12	U37072.1	NT	Human prostate specific antigen gene, 5' flanking region
3421	13358	23143	1.03	2.0E-12	6754495	NT	Mus musculus keratin-associated protein 62 (Krtap-62), mRNA
4025	13328	23704	1.04	2.0E-12	J01884.1	NT	Rat UGA small nuclear RNA
4025	13328	23705	1.04	2.0E-12	J01884.1	NT	Rat UGA small nuclear RNA
4324	14221		1.8	2.0E-12	BE66350.1	EST_HUMAN	CM0-810281-03T109-097-403 B10281 Homo sapiens cDNA
4804	14688	24473	0.78	2.0E-12	U07036	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
4804	14688	24474	0.78	2.0E-12	U07036	SWISSPROT	TBX15 PROTEIN (T-BOX PROTEIN 15)
5658	15804		2.22	2.0E-12	AW971857.1	EST_HUMAN	ES1369346 IMAGE resequences, MAGL Homo sapiens cDNA
6258	16124	28277	3.34	2.0E-12	U07160.1	EST_HUMAN	ES100900 Infant Brain, Bonto Soares Homo sapiens cDNA clone HBB6A13 5' end
6516	16375	26552	2.07	2.0E-12		NT	Homo sapiens Ac- like transposable element (ALT), mRNA
7367	17345		1.98	2.0E-12	AF16984.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein genes, complete cds
7737	17587		8.13	2.0E-12	BE16580.1	EST_HUMAN	Homo sapiens chromosome 21 segment HSZ1C095
9176	18516		1.71	2.0E-12	AI163263.2	NT	Homo sapiens sulfotransferase-related protein (S.L.TX5), mRNA
9377	19041		1.52	2.0E-12	11418248	NT	Homo sapiens sulfotransferase-related protein (S.L.TX5), mRNA
117	10095	19914	1.82	1.0E-12	AW627674.1	EST_HUMAN	Wnt5b107.X1 NCI, CGAP_U12 Homo sapiens cDNA clone IMAGE:2435493 3' similar to contains MER18.11
1944	11830		2.03	1.0E-12	AB81728.1	EST_HUMAN	Wnt5b107.X1 NCI, CGAP_U12 Homo sapiens cDNA clone IMAGE:2435493 3' similar to contains L1.03 L1
3052	12560	22762	1.16	1.0E-12	AF003991.1	NT	repulsive element. Homo sapiens testis-specific, Testis Transcript Y.2 (TTV2) mRNA, partial cds